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Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                      "Construction of a 3-Mb contig and partial transcript map of the central region of mouse chromosome 11."; 3enomics 45:147-157(1997).
                                                  MEDLINE=97480726; PubMed=9339371; DOI=10.1006/geno.1997.4931; Matkins-Chow D.E., Douglas K.R., Buckwalter M.S., Probst F.J.,
                                                                                                            MEDLINE=21354768; PubMed=11461155; DOT=10.1006/mcne.2001.1000;
                             Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                            SEQUENCE OF 1-219 FROM N.A.
                       mouse cDNA sequences."
                                                                 Camper S.A.;
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Hartmann A.M., Rujescu D., Glannakouros T., Nikolakaki E., Goedert M., Mandelkow E.-M., Gao Q.S., Andreadis A., Stamm S.; Ramlation of alternative splicing of human tau exon 10 by phosphorylation of splicing factors."; Mol. Cell. Neurosci. 18:80-90(2001). TISSUE SPECIFICITY, AND MUTAGENESIS OF LYS-189.
MEDLINE=2213485; PubMed=12169639; DOI=10.1074/jbc.M206504200;
Katesu R., Onogi H., Wada K., Kawaguchi Y., Hagiwara M.;
Movel SR-rich-related protein Clasp specifically interacts with inactivated Clk4 and induces the exon EB inclusion of Clk.";
J. Biol. Chem. 277-44220-44228 (2002).

-1- FUNCTION: Phosphorylates serine- and arginine-rich (SR) proteins of the spliceosomal complex may be a constituent of a network of regulatory mechanisms that enable SR proteins to control RNA

splicing. Phosphorylates serines, threonines and tyrosines.
Required for the regulation of alternative splicing of MAPT/TAU.
CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein

tyrosine phosphate.
SUBUNIT: Interacts with UBLS (By similarity).
SUBCELLUIAR LOCATION: Nuclear (By similarity).
ALTERNATIVE PRODUCTS: Event=Alternative splicing; Named isoforms=2;

Isold=035493-1; Sequence=Displayed;

IBold=035493-2; Sequence=VSP 008205; TISSUE SPECIFICITY: Expressed In the hippocampus, the cerebellum

and the olfactorx bulb. PTM: Autophosphorylates on all three types of residues. SIMILARITY: Belongs to the Ser/Thr protein kinase family. Lammer

subfamily.

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InterPro; IPR011009; Kinase like. InterPro; IPR000719; Prot kinase. InterPro; IPR008271; Ser thr pkin AS. InterPro; IPR002290; Ser thr pkinase. Égm: PP00069; Pkinase: I roDom; PD000001; Prot kinase; 1. EMBL; AF033566; AAB87510.1; -. AK013974; BAC25420.1; -. BC002220; AAH02220.1; -. BC012675; AAH12675.1; -. EMBL; U94846; AAB62179.1; fam; PF00069; Pkinase; 4GD; MGI:1098551 SM00220: 200534;

PROSITE; PS00107; PROTEIN KINASE ATP; 1

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Pred. No. 5.1e-132;
8; Mismatches 10;
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ilarity 93.5%;
Conservative &
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Best Local Similarity
Matches 420; Conserv
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MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo. Last sequence update)
Last annotation update) 484 AA (reated) PRT; 01-0CT-2002 (TrEMBLrel. 22, 01-0CT-2002 (TrEMBLrel. 22, 01-MAR-2004 (TrEMBLrel. 26, CDC-like kinase 1. PRELIMINARY; Homo sapiens (Human) SEQUENCE PROM N.A. NCBI\_TaxID=9606; rissum-Bone; Name=CLK1; **Q8N5V8** OBNSVB RESULT 3 **08N5V8** 

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TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION NUMBER: US/10/801/671
CURRENT APPLICATION NUMBER: US/10/801/671
PRIOR PILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: 09/810,671
PRIOR APPLICATION NUMBER: 09/810,671
PRIOR PILING DATE: 2001-03-19
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FRAESEQ for Windows Version 4.0
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Pred. No. 5.8e-170;
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Publication No. US20040152123A1
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Matches 427; Conservative
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US-10-801-671-4
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PROTEIN KINASES AND RELATED PRODUCTS AND METHODS
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Pred. No. 5.2e-166;
8; Mismatches 10; Indels 11;
                               CURRENT APPLICATION NUMBER: US/09/905,999
CURRENT FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: 09/127,248
PRIOR FILING DATE: 1999-07-31
PRIOR FILING DATE: 1997-06-17
PRIOR PILING DATE: 1997-06-17
PRIOR PILING DATE: 1997-06-17
PRIOR PILING DATE: 1997-06-17
PRIOR PILING DATE: 1996-12-19
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PERIOR PRIOR PILING DATE: 1966-12-19
NUMBER OF SEQ ID NOS: 26
SOFTWARE: 28 ALENGTH: 481
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93.5%;
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Matches 420; Conservative
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US-09-905-999-25
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Publication No. US20040071700A1
GENERAL INFORMATION:
APPLICANT: Kim, Jaeseob
APPLICANT: Galant, Ron
ITLE OF INVENTION: Obesity Linked Genes
FILE REFERENCE: LSD-07416
CURRENT APPLICATION NUMBER: US/10/267,502
CURRENT FILING DATE: 2003-01-27
NUMBER OF SEQ ID NOS: 439
SOFTWARE: Patentin version 3.2

SEQ ID NO 355 LENGTH: 481

Sequence 25, Application US/09905999
Patent No. US20020106771A1
GENERAL INFORMATION:
APPLICANT: ULLRICH, Axel
APPLICANT: NAYLER, Oliver

RESULT 10 J

Application US/10267502 o. US20040071700A1

Sequence 355,

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R InterPro; IPR000719; Prot_Kinase.

R InterPro; IPR000271; Ser_thr_pkin.AS.

R InterPro; IPR002271; Ser_thr_pkinase.

R ErdDom; PD000001; Prot kinase; 1.

R SMART; SM00120; ETC; 1.

R ROSITE; PS00101; PROTEIN KINASE ATP; 1.

R ROSITE; PS00101; P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STDPNSVFRCVQMLEWFDHHGHVCIVFELLGLSTYDPIKENSFLPFQIDHIRQMAYQICQ 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SINFLEHINKLITHTDLKPENILFVKSDYVKYNSKAKRDERTLKNTDIKVVDFGSATYDDE 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SKVVECIDHGMDGMHVAVKIVKONVGRYREAARSEIQVLEHLN 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SHYLEARSLNERDYRDRRYVDEYRNDYCEGYVPRHYHRD 56
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                      PTM: Autophosphorylates on all three types of residues. SIMILARITY: Belongs to the Ser/Thr protein kinase family. Lammer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proton acceptor (By similarity).
ATP (By similarity).
K-A: Loss of function.
F#02C36835CDA306 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96.1%; Schre 2315.5; DB 1
96.2%; Pyed. No. 2.3e-135;
ive 2;/ Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          417 RRMLEYDPTORITLDEALQHPFFDLLKKK 445
                                                                                                                                                                                                                                                                   entities requires a license agreement (Se or send an email to license@isb-sib.ch).
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Matches 432; Conservative
                                                                                                                                                                                                                                                                                                                                                                                  HSSP; Q00534; 1B18.
Genew; HGNC:13659; CLK4.
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                                                                                 subfamily
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BINDING
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453 RRMLEYDPTQRITLDEALQHPFFDLLKKK 481

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CENTAINCZECCH II, TISSUB-Breage tumor, C. STRAINCZECCH II, TISSUB-Breage tumor, C. STRAINCZECCH II, TISSUB-Breage tumor, C. STRAINCZECCH II, TISSUB-Breage tumor, C. Strusberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Altenuber R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altechul S.F., Zeeberg B., Barcow K.H., Schaefer C.F., Bhat N.K., Diatchenko L., Marusina K.P., Farmer A.A., Rubin G.M., Hong L., Schuler G.D., Diatchenko L., Marusina K.P., Farmer A.A., Rubin G.M., Hong L., Scheetz T.E., B. Stapletcon M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Rable S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Manlahy J.A., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., May I.J., Hulyk S.W., Vilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Rahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A., Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Makesley R.W., Touchman J.W., Green E.D., Dickson M.C., Abrithe R.M., C., Grimwood J., Schmutz J., Myers R.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kondo S., Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H., Yangaiki Y., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T., Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Baldarelli R., Marapin A., Mateuda H., Batalov S., Balael K.W., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S., Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S., Gasterland T., Gariboldi M., Gissi C., Godzik A., Gough J., Kawaji H., Kawasawa Y., Kedzierski R.M., Kings B.L., Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., Kings B.L., Mantais L., Marchionni L., McKenzie L., Miki H., Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H., Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H., Navasi T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G., Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S., Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K., Varando R., Magner L., Mahlestedt C., Wang Y., Watanabe Y., Wells C., Whilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang I., Yang I., Naraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S., Hirozane-Kishikawa T., Konno H., Makawa T., Kanno H., Nakawa T., Kanno H., Nakawa T., Fukuda S., Haraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S., Harahizume W., Imbanizaki Y., Itoh M., Kagawa I., Nasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Blincy E., Ballaki K., Sabaki D., Shibata K., Shinagawa A., Bahlawa F., Sanda L., Lander E.S., Shinagawa H., Bahlawa F., Sanda D., Shibata K., Shinagawa J., Marana K., Bahlawa F., Shinagara H., Bahlawa F., Bandarith M., Shinada K., Sanda M., Bahlawa F., Bandarith M., Shinada K., Shinagawa H., Bahlawa F., Sasaki D., Sanda M., Bandarith M., Waterston R., Lander E.S., Rogers J., Banda M., Bahlawa F., Sanda K., Sasaki D., Sanda M., Bandarith M., Bandarith M., Bandarith M., Bandarith M., Bandarith M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Analysis of the mouse transcriptome based on functional annotation of
                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM 1).
MEDILINES-9439701.
NAVIER O., Stamm S., Ullrich A.
"Characterization and comparison of four serine- and arginine-rich"
CIK4 MOUSE STANDARD; PRT, 481 AA.
035493; 035721; Q8CEU9; Q95U6;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=C57BL/6J; TISSUE-Head;
MEDLINE-22354683; PubMed=12466851; DOI=10.1038/nature01266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SR) protein kinases.";
Biochem. J. 326:693-700(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                         Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                 like kinase 4).
                                                                                                                                                                                                             Name=Clk4;
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(otqzu) Anola Spoq sint

au Mar 17 11:29:33 2005

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Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.B., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                             FUNCTION.
MEDLINE=21354768; PubMed=11461155; DOI=10.1006/mcne.2001.1000;
Hartmann A.M., Rujescu D., Giannakouros T., Nikolakaki E., Goedert M., Mandelkow E.-M., Gao Q.S., Andreadis A., Stamm S.;
"Regulation of alternative splicing of human tau exon 10 by phosphorylation of splicing factors.";
Mol. Cell. Neurosci. 18:80-90(2001).
                                                                                         "Construction of a 3-Mb contig and partial transcript map of the central region of mouse chromosome 11.";
Genomics 45:147-157(1997).
                                                    SEQUENCE OF 1-219 FROM N.A.
MEDLINE-97480726; PubMed-9339371; DOI=10.1006/geno.1997.4931;
Watkins-Chow D.E., Douglas K.R., Buckwalter M.S., Probst F.J.,
                           and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                SUBUNIT: Interacts with UBL5 (By similarity). SUBCELLULAR LOCATION: Nuclear (By similarity) ALTERNATIVE PRODUCTS:
                                                                                   Camper S.A.;
                                                                                                                                                                                                                                                                                                                                                                         Name=1
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tyrosine phosphate.

Event=Alternative splicing; Named isoforms=2;

IsoId=035493-1; Sequence=Displayed;

IBOId=035493-2; Sequence=VSP 008205;
TISSUE SPECIFICITY: Expressed In the hippocampus, the cerebellum

PTM: Autophosphorylates on all three types of residues. SIMILARITY: Belongs to the Ser/Thr protein kinase family. Lammer

and the olfactorx bulb.

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Pfam; PF00069; Pkinase; I.
ProDom; PD000001; Prot kinase; 1.
SMART; SM00220; S TKC; I.
PROSITE; PS00107; PROTEIN KINASE ATP; 1. MGD, MGI:1099551, Clk4.
InterPro; IPR011009; Kinase like.
InterPro; IPR000719; Prot\_kInase.
InterPro; IPR008271; Ser\_thr\_pkin\_AS.
InterPro; IPR008290; Ser\_thr\_pkin\_ase. EMBL; AF013566; AAB87510.1; -.
EMBL; AK013974; BAC25420.1; -.
EMBL; BC002220; AAH02220.1; -.
EMBL; BC012675; AAH12675.1; -.
EMBL; U94846; AAB62179.1; -.
HSSP; Q00534; IBI8.

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PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00109; PROTEIN_KINASE_ST; 1.
Alternative splicing; ATF-binding; Nuclear protein; Phosphorylation;
Serine/threonine-protein kinase; Transferase; Tyrosine-protein kinase.
                                                                                                                                                                                                                                                                                      57 IESGYRIHCSKSSVRSRRSPKRKRNRHCSSHQSRSKSHRRKRSRSIEDDEEGHLICQSG
                                                                                                                                                                                                                                                                                                                                            117 DVLRARYEIVDTLGEGAFGKVVECIDHGMDGMHVAVKIVKNVGRYREAARSEIQVLEHLN
                                                                                                                                                                                                                                                                                                                                                                                                 153 DVLRARYEIVDTLGEGAFGKVVBCIDHGMDGLHVAVKIVKNVGRYREAARSEIQVLEHLN
                                                                                                                                                                                                                                                                                                                                                                                                                                    177 SIDPNSVFRCVQMLEWFDHHGHVCIVFELLGLSTYDFIKENSFLPFQIDHIRQMAYQICQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                      213 STDPNSVFRCVQMLEWFDHHGHVCIVFELLGLSTYDFIKENSFLPFQIDHIRQMAYQICQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   273 SINFLHHNKLTHTDLKPENILFVKSDYVVKYNSKMKRDERTLKNTDIKVVDFGSATYDDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             333 HHSTLVSTRHYRAPEVILALGWSQPCDVWSIGCILIEYYLGFTVFQTHDSKEHLAMMERI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         237 SINFLHHNKLTHTDLKPENILFVKSDYVVKYNSKMKRDERTLKNTDIKVVDFGSATYDDE
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                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                            11;
                                                   Protein kinase.
ATP (By similarity).
ATP (By similarity).
Proton acceptor (By similarity).
Missing (in isoform 2).
/FIId=VSP 008205.
K->R: Loss of function.
                                                                                                                                                                                                               Score 2261.5; DB 1; Length 481;
Pred. No. 5.1e-132;
8; Mismatches 10; Indels 11;
                                                                                                                                                B -> Q (in Ref. 4).
D -> N (in Ref. 4).
R -> K (in Ref. 2).
F2C56965900C12AA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        445
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TISSUE=Bone;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausnar R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Eukaryota; Metazoa; Chofdata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Pr‡mates; Catarrhini; Hominidae; Homo. Last sequence update)
Last annotation update) 484 AA (reated) 01-OCT-2002 (TrEMBLrel. 22, PRELIMINARY; 01-OCT-2002 (TrEMBLrel. 01-MAR-2004 (TrEMBLrel. Homo sapiens (Human) CDC-like kinase 1. SEQUENCE FROM N.A. NCBI\_TaxID=9606; Name=CLK1; **QBN5VB**; **08N5V8** RESULT 3 

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March 13, 2005, 00:08:08; Search time 138 Seconds (without alignments) 1063.630 Million cell updates/sec
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2410
1 MCIPLEASHSVEEDTHPSHY.....QRITLDEALQHPFFDLLKKK 445
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| Cgn2_6/ptodata/1/pubpaa/US07_BUBCOMB.ppp:*
| Cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.ppp:*
| Cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.ppp:*
| Cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.ppp:*
| Cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.ppp:*
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| Cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.ppp:*
| Cgn2_6/ptodata/1/pubpaa/US106_PUBCOMB.ppp:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SOMMERTES	
Result		Query				
No.	Score	Match	Match Length DB ID	80	QI	Description
-	2410	100.0	445	9	US-09-810-671-2	Sequence 2, Appli
7	2410	100.0	445	13	US-10-109-854-2	Sequence 2, Appli
m	2410	100.0	445	14	US-10-339-656-2	Sequence 2, Appli
4	2410	100.0	445	16	US-10-801-671-2	Sequence 2, Appli
S	2315.5	96.1	481	15	US-10-267-502-352	Sequence 352, App
9	2312	95.9	427	σ	US-09-810-671-4	Sequence 4, Appli
7	2312	95.9	427	13	US-10-109-854-4	Sequence 4, Appli
	2312	95.9	427	14	US-10-339-656-4	Sequence 4, Appli
6	2312	95.9	427	16	US-10-801-671-4	Sequence 4, Appli
10	2261.5	93.8	481	Ø	US-09-905-999-25	Sequence 25, Appl
17	2261.5	93.8	481	15	US-10-267-502-355	Sequence 355, Apr
k	1893	78.5	484	15	US-10-267-502-353	Sequence 353, App
13	1887	78.3	429	0	US-09-810-671-5	Sequence 5, Appli

Sequence Seq Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence	Sequence 20, Appl Sequence 54366, A Sequence 54516, A Sequence 131, App Sequence 539, App Sequence 539, App	Sequence 3, Appl Sequence 3, Appli Sequence 2626, Ap Sequence 351, App Sequence 48, Appl Sequence 23, Appl	Sequence 354, App Sequence 350, App Sequence 350, App Sequence 4699, Ap Sequence 349, App Sequence 315, App	Sequence 53826, A Sequence 53826, A Sequence 52391, A Sequence 55309, A Sequence 45337, A Sequence 179828, Sequence 67650, A
S-10-109-85 S-10-339-65 S-10-801-67 S-10-116-27 S-10-755-88	9 US-09-905-999-20 15 US-10-425-114-54316 15 US-10-425-114-54310 16 US-10-664-421-131 15 US-10-267-502-357 9 US-09-925-298-539 14 US-10-102-806-539	9 US-09-905-999-21 10 US-09-790-823-3 115 US-10-104-047-2626 115 US-10-164-502-351 115 US-10-182-243-48 115 US-09-905-999-23	US-10-267- US-10-425- US-10-267- US-10-108- US-10-267- US-10-267-	15 US-10-425-114-51418 15 US-10-425-114-51326 15 US-10-425-114-52391 15 US-10-425-114-55309 15 US-10-425-114-45337 16 US-10-437-963-179828 15 US-10-425-114-67650
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## ALIGNMENTS

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APPLICANT: YAN, Chunhua et al
APPLICANT: YAN, Chunhua et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: HERROF
FILE REFERENCE: CLOO0758
CURRENT APPLICATION NUMBER: US/09/810,671
CURRENT PILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 445
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             Sequence 2, Application US/09810671 Publication No. US20020076783A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Human
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US-09-810-671-2
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Sequence 2, Application US/10339656
| Pubblication No. US20030134319A1
| GENERAL INFORMATION:
| TUBLICATION:
| TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
| TITLE OF INVENTION: THEREOF
| TITLE OF INVENTION: THEREOF
| TITLE OF INVENTION: THEREOF
| TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
| TITLE OF INVENTION: THEREOF
| FILE REFERENCE: CLOOOTSBDIV2
| CURRENT APPLICATION NUMBER: US/10/339,656
| CURRENT FILING DATE: 2003-04-01
| PRIOR APPLICATION NUMBER: 09/810,671
| PRIOR FILING DATE: 2001-03-19
| PRIOR FILING DATE: 2001-03-19
| PRIOR FILING DATE: 2000-08-24
| NUMBER OF SEQ ID NOS: 5
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 2
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                           361 PQHMIQKTRKRKYFHHNQLDWDEHSSAGRYVRRRCKPLKEFMLCHDEEHEKLFDLVRRML 420
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Best Local Similarity 100.0%; Pred. No. 1.7e-177;
Matches 445; Conservative 0; Mismatches 0;
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ORGANISM: Homo sapien
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Publication No. US20020119548A1

GENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS,
TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

CURRENT APPLICATION NUMBER: US/10/109,854

CURRENT FILING DATE: 2002-04-01

PRIOR APPLICATION NUMBER: 09/227,470

PRIOR PELING DATE: 2001-08-24

PRIOR PELING DATE: 2001-08-24

PRIOR FILING DATE: 2001-03-19

NUMBER OF SEQ ID NOS: 5

SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                       LHHNKLTHTDLKPENI LFVKSDYVVKYNSKMKRDERTLKNTDI KVVDFGSATYDDEHHST
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100.0%; Score 2410; DB 13; Length 445;
Best Local Similarity 100.0%; Pred. No. 1.7e-177;
Matches 445; Conservative 0; Mismatches 0; Indels 0;
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TYPE: PRT
ORGANISM: Homo sapiens
US-10-267-502-352
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US-09-810-671-4
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; SEQ ID NO 352
; LENGTH: 481
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Matches 42
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        Sequence 2, Application US/10801671

Publication No. US20040152123A1

GENERAL INFORMATION:

APPLICANT: YAN, Chunhua et al.

TITLE OF INVENTION: ISCLATED HUMAN KINASE PROTEINS, NUCLEIC

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

TITLE OF INVENTION: US/10/801,671

CURRENT PELING DATE: 2004-03-17

FILE REFERENCE: CLO00758DIV-III

CURRENT APPLICATION NUMBER: 06/227,470

PRIOR APPLICATION NUMBER: 09/810,671

PRIOR PILING DATE: 2000-08-24

PRIOR PILING DATE: 2001-03-19

NUMBER OF SEQ ID NOS: SOFTWARE: PARKEN FARENCE PARKENCE PARKENCE
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Sequence 352, Application US/10267502

Publication No. US20040071700A1

GENERAL INFORMATION:
APPLICANT: Kim, Jaeseob
APPLICANT: Kim, Jaeseob
TITLE OF INVENTION:
FILE REFERENCE: LSD-07416
CURRENT APPLICATION NUMBER: US/10/267,502
CURRENT APPLICATION NUMBER: US/10/267,502
CURRENT FILING DATE: 2003-01-27

WUMBER OF SEQ ID NOS: 439

SOFTWARE: PatentIn version 3.2
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Best Local Similarity
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Sequence 4, Application US/09810671
| Publication No. US20020076783A1
| Publication No. US20020076783A1
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
| TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
| TITLE OF INVENTION: THEREOF
| FILE REFERENCE: CLO00758
| CURRENT APPLICATION NUMBER: US/09/810,671
| CURRENT PILING DATE: 2001-06-08
| NUMBER OF SEQ ID NOS: 5
| SOFTWARE: FastSEQ for Windows Version 4.0
| TENCHAL A.7
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Score 2315.5; DB 15; Length 481;
Pred. No. 3.6e-170;
2; Mismatches 4; Indels 11;
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    96.1%;
                           Best Local Similarity 96.2
Matches 432; Conservative
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420

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TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES;
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES;
TITLE OF INVENTION: THEREOF;
TURENT PAPPLICATION NUMBER: US/10/339,656
CURRENT APPLICATION NUMBER: 10/109,854
PRIOR APPLICATION NUMBER: 09/109,854
PRIOR PLING DATE: 2002-04-01
PRIOR PLING DATE: 2001-03-19
PRIOR PLING DATE: 2001-03-19
PRIOR PLING DATE: 2001-03-19
PRIOR PLING DATE: 2001-03-19
PRIOR APPLICATION NUMBER: 60/227,470
PRIOR APPLICATION NUMBER: 60/227,470
PRIOR PRIOR APPLICATION NUMBER: 5001-03-19
PRIOR PRIOR DATE: 2001-03-19
PRIOR PRIOR APPLICATION NUMBER: 5001-03-19
PRIOR PRIOR APPLICATION NUMBER: 60/227,470
PRIOR APPLICATION NUMBER: 5001-03-19
PRIOR APPLICATION NUMBER: 5001-03-19
PRIOR APPLICATION NUMBER: 5001-03-19
PRIOR APPLICATION NUMBER: 5001-03-19
                                                                         SQPCDVWSIGCILIEYYLGFTVFQTHDSKEHLAMMERILGFIPQHMIQKTRKRKYFHHNQ 360
      241 VKSDYVVKYNSKMKRDERTLKNTDIKVVDFGSATYDDEHHSTLVSTRHYRAPEVILALGW 300
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                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/10339656
Publication No. US20030134319A1
                                                                                                                                                                                                                  FDLLKKK 445
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; ORGANISM: Homo sapien
US-10-339-656-4
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421 FDLLKKK 427
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Sequence 4, Application US/10109854

Bublication No. US20020119548A1

GENERAL INFORMATION

TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS,

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS,

CURRENT PEPELCATION NUMBER: US/10/109,854

CURRENT PEPELCATION NUMBER: 60/227,470

PRIOR FILING DATE: 2000-08-24

PRIOR FILING DATE: 2001-03-19

NUMBER OF SEQ ID NOS: 5

SOFTWARE FASTSEQ for Windows Version 4.0
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                                                                                  ECIDHGMDGMHVAVKI VKNVGRYREAARSEIQVLEHLNSTDPNSVFRCVQMLEWFDHHGH
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100.0%; Pred. No. 5.8e-170;
tive 0; Mismatches 0;
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US-10-109-854-4
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Best Local Similarity
Matches 427; Conserv
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LENGTH: 427
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US-10-267-502-355
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                                                                                                             Sequence 4, Application US/10801671
| Publication No. US20040152123A1
| GENERAL INFORMATION: US20040152123A1
| GENERAL INFORMATION: US20040152123A1
| APPLICANT: YAN, Chunhua et al.
| TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
| TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS,
| TITLE OF INVENTION: THEREOF
| FILE REFERENCE: CL000758DIV-III
| CURRENT APPLICATION NUMBER: US/10/801,671
| PRIOR APPLICATION NUMBER: 60/227,470
| PRIOR APPLICATION NUMBER: 09/810,671
| PRIOR FILING DATE: 2000-08-24
| NUMBER OF SEQ ID NOS: 5
| SOFTWARE: FastSEQ for Windows Version 4.0
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Patent No. US20020106771A1
GENERAL INFORMATION:
APPLICANT: ULLRICH, Axel
APPLICANT: NAYLER, Oliver
                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
FDLLKKK 445
                                FDLLKKK 427
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        213 STDFNSVFRCVQMLEWFDHHGHVCIVFELLGLSTYDFIKENSFLPFQIDHIRQMAYQICQ 272
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TITLE OF INVENTION: CLK PROTEIN KINASES AND RELATED PRODUCTS AND METHODS
FILE REFERENCE: 038602/0431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57 IESGYRIHCSKSSVRSRRSSPKRKRNRHCSSHQSRSKSHRRKRSRSIEDDEEGHLICQSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STDPNSVFRCVQMLEWFDHHGHVCIVFELLGLSTYDFIKENSFLPFQIDHIRQMAYQICQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 481;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 2261.5; DB 9,
Pred. No. 5.2e-166;
8; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 355, Application US/10267502; Publication No. US20040071700A1; GENERAL INFORMATION:
APPLICANT: Kim, Jaeseob; APPLICANT: Kim, Jaeseob; APPLICANT: Galant, Ron TITLE OF INVENTION: Obesity Linked Genes; FILE REFERENCE: LSD-07416; CURRENT APPLICATION NUMBER: US/10/267,502; CURRENT PILING DATE: 2003-01-27; NUMBER OF SEQ ID NOS: 439; SOFTWARE: Patentin version 3.2; SEQ ID NO 355; LENGTH: 481
                                   FILE KEFAKEAL USACZ/V43.

CURRENT FILING DATE: 2001-07-17

PRIOR APPLICATION NUMBER: 09/127,248

PRIOR FILING DATE: 1990-07-31

PRIOR PILING DATE: 1999-07-31

PRIOR PILING DATE: 1997-06-17

PRIOR PILING DATE: 1997-06-17

PRIOR FILING DATE: 1997-06-17

PRIOR FILING DATE: 1997-06-17

PRIOR PILING DATE: 1997-06-17

PRIOR PILING DATE: 1996-12-19

NUMBER OF SEQ ID NOS: 26

SEQ ID NO 25
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93.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 420; Conservative
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; ORGANISM: Mus musculus
US-09-905-999-25
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Sequence 5, Application US/09810671

Publication No. US20020076783A1

GENERAL INFORMATION:

APPLICANT: YAN, Chunhua et al

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

FILE REPERENCE: CLOO0758

CURRENT APPLICATION NUMBER: US/09/810,671

CURRENT FILING DATE: 2001-06-08

NUMBER OF SEQ ID NOS: 5

SOFTWARE: FRACSEQ for Windows Version 4.0

SEQ ID NO 5
                                                                                                                                                                     174 KVVECIDHKAGGRHVAVKIVKNVDRYCEAARSEIQVLEHLNTTDPNSTFRCVQMLEWFEH 233
                                                                                            ILFVKSDYVVKYNSKMKRDERTLKNTDIKVVDFGSATYDDEHHSTLVSTRHYRAPEVILA 315
                                                                                                                                                                                                                   435
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                                                     376 HNQLDWDEHSSAGRYVRRRCKPLKEFWLCHDEEHEKLFDLVRRMLEYDPTQRITLDEALQ
                                                                                                                                                      LGWSQPCDVWSIGCILIEYYLGFTVFQTHDSKEHLAMMERILGPIPQHMIQKTRKRKYFH
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82.1%; Pred. No. 3.4e-137;
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Best Local Similarity 82.1*
Matches 352; Conservative
                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Human
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                                                                                                                   8 SH-SVEEDTH-----PSHYLEARSINERDYRDRRYVDEYRNDYCEGYVPRHYHRD
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                                            Score 2261.5; DB 15; Length 481;
Pred. No. 5.2e-166;
8; Mismatches 10; Indels 11;
                                                                            11;
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82.3%; Pred. No. 1.4e-137;
live 30; Mismatches 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RRMLEYDPTQRITLDEALQHPFFDLLKKK 445
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Publication No. US20040071700A1
Publication No. US20040071700A1
PAPLICANT: Kim, Jaeseob
PPLICANT: Galant, Ron
FILE REFERENCE: LSD-07416
CURRENT APPLICATION NUMBER: US/10/267,502
CURRENT APPLICATION NUMBER: US/10/267,502
NUMBER OF SEQ ID NOS: 439
SOFTWARE: PatentIn version 3.2
LENGTH: 484
                                            93.8%;
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Best Local Similarity 82.3%
Matches 353, Conservative
                                                                      Matches 420; Conservative
; ORGANISM: Mus musculus
US-10-267-502-355
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ORGANISM: Homo sapiens
                                       Query Match
Best Local Similarity
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US-10-267-502-353
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US-10-267-502-353
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TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THERROF
TITLE OF INVENTION: THERROF
FILE REFERENCE: CLOOO758DIV2
CURRENT APPLICATION NUMBER: US/10/339,656
CURRENT PILING DATE: 2003-01-10
PRIOR APPLICATION NUMBER: 10/109,854
PRIOR PELING DATE: 2002-04-01
PRIOR PELING DATE: 2001-03-19
PRIOR FILING DATE: 2001-03-19
PRIOR FILING DATE: 2000-08-24
NUMBER OF SEQ ID NOS: 5
SEQ ID NO 5
LENGTH: 429
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US-10-109-854-5
Sequence 5, Application US/10109854
Sequence 5, Application WS/10109854
Sequence 5, Application No. US2020119548A1
Sequence 5, Application No. US2020119548A1
SERNET NO. US2020119548A1
TITLE OF INVENTION: SCLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
CURRENT APPLICATION NUMBER: US/10/109,854
CURRENT APPLICATION NUMBER: 60/227,470
PRIOR PILING DATE: 2000-08-24
PRIOR FILING DATE: 2000-08-24
PRIOR FILING DATE: 2001-03-19
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78 KRK-RNRHCSSH-QSRSKSHRRKRSRSIEDDEEGHLICQSGDVLRARYEIVDTLGEGAFG 135
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78.3%; Score 1887; DB 13;
Best Local Similarity 82.1%; Pred. No. 3.4e-137;
Matches 352; Conservative 30; Mismatches 45;
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US-10-339-656-5
i. Sequence 5, Application US/10339656
i. Publication No. US20030134319A1
j. GENERAL INFORMATION:
                                                                                     HPFFDLLKK 429
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                                                    HPFFDLLKK 444
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US-10-109-854-5
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                                                                                                                                                                                 1 SHYLESRSINEKDYHSRRYIDEYRNDYTQGCEPGHRQRDHESRYQNHSSKSSGRSGRSSY
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                                                                                                                                                          18 SHYLEARSLNERDYRDRRYVDEYRNDYCEGYVPRHYHRDIESGYRIHCSKSSVRSRRSSP
                                                                     Length 429;
                                                                                                            Indels
                                                              tch 78.3%; Score 1887; DB 14; al Similarity 82.1%; Pred. No. 3.4e-137; 352; Conservative 30; Mismatches 45;
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, ORGANISM: Homo sapien
US-10-339-656-5
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

March 12, 2005, 23:51:06; Search time 170 Seconds (without alignments) 1340.443 Million cell updates/sec

Title: Perfect score: Sequence:

US-10-801-671-2
2410
MCIPLEASHSVEEDTHPSHY.....QRITLDEALQHPFFDLLKKK 445

Scoring table:

1612378 seqs, 512079187 residues BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

1612378 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt\_03:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	Oghazl homo gapien	-	Q8n5v8 homo sapien	_	Q9bggl macaca fasc	22518 mus musculu	Q9nr16 homo sapien		Q91yr2 mus musculu	_	P49760 homo sapien	Q7zy59 xenopus lae	_	Q63117 rattus norv	Q6irk2 rattus norv	35492 mus musculu	Q8clv1 mus musculu		-				Q7pqg8 anopheles g	17917 caenorhabdi	Q8mly2 caenorhabdi		P51567 arabidopsis		P51566 arabidopsis	2943m7 oryza sativ	51568 arabidopsis
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SOMETHIES	CLK4 HUMAN	CLK4_MOUSE	Q8N5V8	CLK1_HUMAN	Q9BGQ1	CLK1_MOUSE	Q9NRL6	Q6AYK7	Q91YR2	CLK2_MOUSE	CLK2_HUMAN	Q72Y59	CLK3_HUMAN	CLK3_RAT	Q61RK2	CLK3_MOUSE	Q8C1V1	Q9BRG8	DOA_DROME	Q86 <u>B</u> 73	Q7PNI9	Q7Q4W1	Q7PQG8	017917	Q8MLY2	Q7PH65	AFC2 ARATH	049967	AFC1 ARATH	Q943M7	AFC3_ARATH
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* Query Match	.96.1	93.8	78.5	78.3	78.0	76.0	74.8	66.7	59.6	59.5	58.8	58.0	54.8	54.6	54.6	54.4	54.1	52.0	49.0	49.0	46.6	46.4	42.0	40.2	40.0	36.7	35.2	34.8	34.4	33.3	32.8
Score	2315.5	2261.5	1893	1887	1879	1832	1803	1608	1437	1427.5	1417	1398	1321	1317	1316	1310	1305	1252	1180	1180	1122	1119	101	969.5	963	884.5	848.5	839	830	802	790
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## ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R InterPro; IPRO11009; Kinase like.

R InterPro; IPRO00719; Prot_kinase.

R InterPro; IPRO00271; Ser_thr_pkin_AS.

R InterPro; IPRO02201; Ser_thr_pkin_AS.

R InterPro; IPRO02201; Ser_thr_pkinase.

R Probom; PD000001; Prot_kinase; I.

R PROSITE; PS001007; PROTEIN_KINASE_DAD; I.

R PROSITE; PS001007; PROTEIN_KINASE_DAD; I.

R PROSITE; PS001009; PROTEIN_KINASE_DAD, I.

R PROSITE; PS001009; PROTEIN_KINASE_DAD, I.

R PROSITE; PROGOTO PROTEIN_KINASE_DAD, I.

R PROSITE, PROGOTO PROTEIN_KINASE_DAD, I.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            153 DVLRARYEIVDTLGEGAFGKVVECIDHGMDGMHVAVKIVKNVGRYREAARSEIQVLEHLN 212
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                           PTM: Autophosphorylates on all three types of residues. SIMILARITY: Belongs to the Ser/Thr protein kinase family. Lammer
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96.2%; Pred. No. 2.3e-135;
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Genew, HGNC:13659; CLK4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDILINE=22313485; PubMed=12165633; DOI=10.1074/jbc.M206504200;
A Katsu R., Onogi H., Wada X., Kawaguchi Y., Hagiwara M.;
T "Novel SR-rich-related protein Clasp specifically interacts with
I inactivated Clk4 and induces the exon EB inclusion of Clk.";
J. Biol. Chem. 277:44220-44228 (2002).

-1- FUNCTION: Phosphorylates serine- and arginine-rich (SR) proteins of the splicesomal complex may be a constituent of a network of regulatory mechanisms that enable SR proteins to control RNA splicing. Phosphorylates serines, threonines and tyrosines.

C Required for the regulation of alternative splicing of MAPT/TAU.

-1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.

C -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein

C -1- SUBGUILT: Interactes with UBL5 (By similarity).

-1- ALTERNATIVE PRODUCTS:
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                      MEDLINE=21354768; PubMed=11461155; DOI=10.1006/mcne.2001.1000; Hartmann A.M., Rujescu D., Giannakouros T., Nikolakaki E., Goedert M., Mandelkow E., M., Gao Q.S., Andreadis A., Stamm S.; Regulation of alternative splicing of human tau exon 10 by phosphorylation of splicing factors.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isold=035493-2; Sequence=VSP 008205; TISSUE SPECIFICITY: Expressed in the hippocampus, the cerebellum and the olfactorx bulb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PTM: Autophosphorylates on all three types of residues. SIMILARITY: Belongs to the Ser/Thr protein kinase family. Lammer
                                                                                                                                                                                                       "Construction of a 3-Mb contig and partial transcript map of the central region of mouse chromosome 11."; Genomics 45:147-157(1997).
                                                                                                     [4]
SEQUENCE OF 1-219 FROM N.A.
MEDLINE=97480726; PubMed=9339371; DOI=10.1006/geno.1997.4931;
Watkins-Chow D.B., Douglas K.R., Buckwalter M.S., Probst F.J.,
                                                             and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AND MUTAGENESIS OF LYS-189.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGD; MGI:1099551; Clk4.
InterPro; IPR011009; Kinase like.
InterPro; IPR001009; Kinase like.
InterPro; IPR000719; Prot kinase.
InterPro; IPR002290; Ser_thr_pkin AS.
InterPro; IPR002290; Ser_thr_pkināse.
Fēm; PF00069; Pkinase; I.
FroDom; PD000001; Prot kinase; I.
SWART; SM00220; S. TKC; I.
PROSITE; PS00107; PROTEIN_KINASE_ATP; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IsoId=035493-1; Sequence=Displayed;
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237 SINFLHHNKLTHTDLKPENILFVKSDYVVKYNSKMKRDERTLKNTDIKVVDFGSATYDDE 296
273 SINFLHHNKLTHTDLKPENILFVKSDYVVKYNSKMKRDERTLKNTDIKVVDFGSATYDDE 332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                     11;
                                                                                                                                                                                            Score 2261.5; DB 1; Length 481;
Pred. No. 5.1e-132;
8; Mismatches 10; Indels 11;
                                                                                                                                                                      57344 MW; F2C56965900C12AA CRC64;
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Last annotation update)
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01-OCT-2002 (TrEMBLrel. 22,
01-MAR-2004 (TrEMBLrel. 26,
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Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,
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A. Richards S., Wolferd W., Soarcia A.M., Gay L.J., Hulyk S.W.,
Yillalon D.K., Muzny D.M., Soarcia A.M., Gay L.J., Hulyk S.W.,
A. Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
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A. Const S.J., Marra M.A.;
A. Jones S.J., Marra M.A.;
A. Gones S.J., Marra M.A.;
A. Gones S.J., Marra M.A.;
A. Gones C.J., Marra M.A.;
A. Gones C.J., Marra M.A.;
A. Dickson W. Sequences.,
A. Droc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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R GO; GO:0005524; F:ATP binding; IEA.

R GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.

R GO; GO:0006469; F:ransferase activity; IEA.

GO; GO:0006469; P:protein amino acid phosphorylation; IEA.

R InterPro; IPR001009; Kinase like.

R InterPro; IPR00220; Ser_thr_pkinase.

R InterPro; IPR00221; Ser_thr_pkinase.

R InterPro; IPR005271; Ser_thr_pkinase.

R Promo; PP0000001; Prote kinase; 1.

R PROSITE; PS00107; PROTEIN KINASE ATP; 1.

R PROSITE; PS00107; PROTEIN KINASE DOM; 1.

R PROSITE; PS00109; PROTEIN KINASE ST; UNKNOWN 1.

W ATP-binding; Kinase; Transferase.

C SEQUENCE 484 AA; 57290 MW; F34B5B4498BBD118 CRC64;
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Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC031549; AAH31549.1; --
HSSP; Q00534; 1BI8.
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Matches 353; Conservative 3
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                      01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last sequence update)
05-0TL-2004 (Rel. 34, Last amnotation update)
Dual specificity protein kinase CLK1 (EC 2.7.1.37) (EC 2.7.1.112) (CDC like kinase LN shanase CLK1; Synonyma=CLK; Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=P49759-2; Sequence=VSP_004852, VSP_004853;
Note=Lacks the kinase domain. May be produced at very low levels due to a premature stop codon in the mRNA, leading to nonsense-mediated mRNA decay;
                                                                                                                                                                                                                                                                                                                                                                                                      Johnson K.W., Smith K.A.; "Molecular cloning of a novel human cdc2/CDC28-like protein kinase."; J. Biol. Chem. 266:3402-3407(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=1759258; DOT=10.1186/gb-2004-5-2-78;

Hillman R.T., Green R.E., Brenner S.E.;

"An unappreciated role for RNA surveillance.";

Genome Biol. 5:RESEARCH081.-RESEARCH081.6(2004).

-!- FUNCTION: Phosphorylates serine- and arginine-rich (SR) proteins of the spliceosomal complex may be a constituent of a network of regulatory mechanisms that enable SR proteins to control RNA splicing. Phosphorylates serines, threonines and tyrosines (By shillsty).

-!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.

-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE-55082033; PubMed=7990150;
Hanes J.J., der Kammer H., Klaudiny J.J., Scheit K.H.;
Hanes J.J., der Kammer H., Klaudiny J.J., Scheit K.H.;
Flancacterization by cDNA cloning of two new human protein kinases.
Evidence by sequence comparison of a new family of mammalian protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. Lammer
                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- PTM: Autophosphorylates on all three types of residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPLICE ISOFORM(S) THAT ARE POTENTIAL NMD TARGET(S)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Event=Alternative splicing; Named isoforms=2;
                                                                                                   484 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IsoId=P49759-1; Sequence=Displayed;
                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tyrosine phosphate.
-- SUBUNIT: Interacts with PPIG.
--- SUBCELLULAR LOCATION: Nuclear
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=91139618; PubMed=1704889;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mol. Biol. 244:665-672(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; L29219; AAA61480.1; -. EMBL; L29222; AAB59459.1; -.
                                                                                                   STANDARD;
474 HPFFDLLKK 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   similarity).
                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
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                                                                              CLK1 HUMAN
ID CLK1 HUMAN
AC P49759;
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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us-10-801-671-2.rup

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94 ESRYQNHSSKSSGRSGRSSYKSKGRIHHSTSHRRSHGKSHRRKRTRSVEDDEEGHLICQS 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34 SHSSARENKRCKYTHSKMCDSHYLESRCINEKDYRSRRYIDEYRNDYNQECEPGHRHRDH 93
                                                                                                                                                                                                                                M., Terao K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        154 GDVLSARYEIVDALGEGAFGKVVECIDHKAGGRHVAVKIVKNVDRYCEAARSEIQVLEHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                176 NSTDPNSVFRCVQMLEWFDHHGHVCIVPELLGLSTYDFIKENSFLPFQIDHIRQMAYQIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        214 NTTDPNSTFRCVQMLEWFEHHGHICIVFELLGLSTYDFIKENGFLPFRLDHIRKMAYQIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        334 EHHSTLVSTRHYRAPEVILALGWSQPCDVWSIGCILIBYYLGFTVFPTHDSKEHLAMMER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SHSVEED----TH----PSHYLEARSLNERDYRDRRYVDEYRNDYCEGYVPRHYHRDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58 ESGYRIHCSKSSVRSRRSSPKRK-RNRHCSSH-QSRSKSHRRKRSRSIEDDEEGHLICQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  236 QSINFLHHNKLTHTDLKPENILFVKSDYVVKYNSKMKRDERTLKNTDIKVVDFGSATYDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EHHSTLVSTRHYRAPEVILALGWSQPCDVWSIGCILIEYYLGFTVFQTHDSKEHLAMMER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12; Gaps
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypochetical protein.
Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                         ROUGH CONTROLL FATP binding; IEA.

GO; GO: 000554; FaTP binding; IEA.

GO; GO: 0004674; F: Protein serine/threonine kinase activity; IEA.

GO; GO: 00016740; F: transferase activity; IEA.

R GO; GO: 00016740; F: transferase activity; IEA.

GO; GO: 00016740; F: transferase activity; IEA.

R GO; GO: 0006468; P: protein amino acid phosphorylation; IEA.

InterPro; IPR01009; Rinase like.

R InterPro; IPR000719; Prot Kinase.

R InterPro; IPR0008270; Ser thr pkinase.

R Probom; PD000001; Prot Kinase; I.

R PROSITE; PS00107; PROTEIN KINASE ATP; I.

R PROSITE; PS00107; PROTEIN KINASE DOM; I.

R PROSITE; PS00108; PROTEIN KINASE ST; UNKNOWN I.

R PROSITE; PS00108; PROTEIN KINASE ST; UNKNOWN I.

R ATP-binding; Hypothetical protein; Kinase; Transferase.

SEQUENCE 484 AA; 57318 MW; F5324D4007119878 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 484;
                                                                                                                                                                                                      TISSUB-Frontal lobe left, Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai Suzuki Y., Sugano S., Hashimoto K.; Submitted (FEB-2001) to the BMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
78.0%; Score 1879; DB 2;
Best Local Similarity 79.3%; Pred. No. 2.3e-108;
Matches 356; Conservative 30; Mismatches 51;
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                                                                                                                                                                                                                                                                                         EMBL; AB056421; BAB33079.1; -. HSSP; Q00534; 1BI8.
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                                                                                                                             Cercopithecinae, Macaca
                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                NCBI TaxID=9541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 6
CLK1_MOUSE
ID _CLK1_MOUSE
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                                                   H-InvDB; HIXO002128; --

R MIM; 601951; --

R GO; GO:0004715; F:non-membrane spanning protein tyrosine kina. ..; TAS.

GO; GO:0004715; F:non-membrane spanning protein tyrosine kina. ..; TAS.

GO; GO:000674; F:protein serine/threonine kinase activity; TAS.

R GO; GO:000074; P:regulation of cell cycle; TAS.

R GO; GO:000074; P:regulation of cell cycle; TAS.

R InterPro; IPR00019; F:regulation of cell cycle; TAS.

InterPro; IPR000211; Ser thr pkin AS.

R InterPro; IPR002201; Ser thr pkin AS.

R InterPro; IPR001019; Prot kinase; I.

R Prom; PD000001; Prot kinase; I.

R SWART; SM00220; S TKC; I.

R PROSITE; PS00101; PROTEIN KINASE ATP; I.

R PROSITE; PS00108; PROTEIN KINASE BTP; I.

R PROSITE; PS00108; PROTEIN KINASE ST; I.

R Alternative splicing; ATP-binding; Nuclear protein; Phosphorylation;

SCATIES/threonine-protein kinase; Transferase; Tyrosine-protein kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | KOVECIDHGMDGMHVAVXIVKNVGRYREAARSEIQVLEHLNSTDPNSVFRCVQMLEWFDH 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           255
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein kinase.
ATP (By similarity).
ATP (By similarity).
Proton acceptor (By similarity).
FYSHRRK -> MYLLIL (in isoform Short).
/FTId=VSP_004852.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78.3%; Score 1887; DB 1; Length 484; 82.1%; Pred. No. 7.4e-109; ive 30; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Missing (In isoform Short) /FIId=VSP_004853.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            484 AA; 57205 MW; 304B5B4486AD0A6B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 82.13
Matches 352, Conservative
PIR; SS3641; SS3641.
HSSP; Q00534; 1BI8.
Genew; HGNC:2068; CLKI.
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HPFFDLLKK 482
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BINDING
ACT SITE
VARSPLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48 HSKTTD---SYYLESRSINEKAYHSRRYVDEYRNDYM-GYEPGHPYGEPGSRYQMHSSKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69 SVRSRRSSPXRK-RNR-HCSSHQSRSKSHRRKRSRSIEDDEEGHLICQSGDVLRARYEIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 164 DILGEGAFGKVVECIDHKVGGRRVAVKIVKNVDRYCEAAQSEIQVLEHLNTIDPHSIFRC
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and for
Usage by
   modified and this statement is not removed.
                            entities requires a license agreement ( or send an email to license@isb-sib.ch)
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                                                                                                               EMBL, X57186; CAA40473.1; --
EMBL, M83811, AAA40151.1; --
EMBL, U21209; AAC52257.1; --
EMBL, L29221; AAA61485.1; --
EMBL, L39275; L39275;
PIR, 149275; 149275;
HSSP, Q00534; 1B18
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                                                                                                                        CDC
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1801d=2518-2; Sequence=VSP_004854, VSP_004855;
Note=Lacks the kinase domain;
PTM: Autophosphorylates on all three types of residues.
SIMILARITY: Belongs to the Ser/Thr protein kinase family. Lammer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    regulates their intranuclear distribution.";

EMBO J. 15:265-275(1996).

-!- FUNCTION: Phosphorylates serine- and arginine-rich (SR) proteins of the spliceosonal complex may be a constituent of a network of regulatory mechanisms that enable SR proteins to control RNA splicing. Phosphorylates serines, threonines and tyrosines.
-!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORM SHORT).
MEDLINE-55082033; PubMed=7990150;
Hanes J.J., der Kammer H., Klaudiny J.J., Scheit K.H.;
Hanes J.J., der Kammer H., Klaudiny J.J., Scheit K.H.;
Entarcterization by CDNA cloning of two new human protein kinases.
Evidence by sequence comparison of a new family of mammalian protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Colwill K., Pawson T., Andrews B., Prasad J., Manley J.L., Bell J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               D.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Alternative splicing of STY, a nuclear dual specificity kinase.";
J. Biol. Chem. 270:21524-21531(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The Clk/Sty protein kinase phosphorylates SR splicing factors and
                         01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
05-JUL-2004 (Rel. 19, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Dual specificity protein kinase CLK1 (EC 2.7.1.37) (EC 2.7.1.112)
like kinase 1) (Protein kinase STY).
Mane-clk1; Synonyms=Clk, STY;
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=91122038; PubMed=1825055;
Ben-David Y., Letwin K., Tannock L., Bernstein A., Pawson T.;
A mammalian protein kinase with potential for serine/threonine tyrosine phosphorylation is related to cell cycle regulators.";
EMBO J. 10:317-325(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM SHORT).
MEDLINE=95394904; PubMed=7665564; DOI=10.1074/jbc.270.37.21524;
Duncan P.I., Howell B.W., Marius R.M., Drmanic S., Douville E.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=91094875; PubMed=1986248;
Howell B.W., Afar D.E., Lew J., Douville E.M., Icely P.L., Gray
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "STY, a tyrosine-phosphorylating enzyme with sequence homology serine/threonine kinases.";
Mol. Cell. Biol. 11:568-572(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tyrosine phosphate.
SUBUNIT: Interacts with PPIG (By similarity).
SUBCELLUIAR LOCATION: Nuclear.
SUBERNATIVE PRODUCTS:
Event-Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=Long;
IsoId=P22518-1; Sequence=Displayed;
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CHARACTERIZATION.
MEDLINE-96178222; PubMed=8617202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mol. Biol. 244:665-672(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
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Bell J.C.;

Bell J.C.;

Duncan P.I

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Query Match
Best Local Similarity 98.7
Matches 297; Conservative
                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Director MGC Project;
  446 FFDLLKKK 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein.
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                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Testis;
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                                                                                                                     Q6AYK7
                                                                        RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               326 WSQPCDVWSIGGIIJNEYYLGFTVFQTHDSKEHLAMMERILGPIPQHMIQKTRKRKYFHHN 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           386 QLDWDEHSSAGRYVRRRCKPLKEFMLCHDEEHEKLFDLVRRMLEYDPTQRITLDEALQHP 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 146 VECIDHKAGGRHVAVKIVKAVDRYCEAARSEIQVLEHLNTTDPNSTFRCVQMLEWFEHHG 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KRKRNRHCSSHQSRSKSHRRKRSRSIEDDEEGHLICQSGDVLRARYEIVDTLGEGAFGKV 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         114 KSKHRIH-----HSTSHRRSH------GD-----EIVDTLGEGAFGKV 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VECIDHGMDGMHVAVKIVKNVGRYREAARSEIQVLEHLNSTDPNSVFRCVQMLEWFDHHG 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FVKSDYVVKYNSKMKRDERTLKNTDIKVVDFGSATYDDEHHSTLVSTRHYRAPEVILALG 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WSQPCDVWSIGCILIEYYLGFTVFQTHDSKEHLAMMERILGPIPQHMIQKTRKRKYFHHN 377
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                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    G0:0005524; F.ATP binding; IEA.
G0:0004674; F.protein serine/threonine kinase activity; IEA.
G0:0016740; F.transferase activity; IEA.
G0:0006468; P.protein amino acid phosphorylation; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 453;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 74.8%; Score 1803; DB 2; Length 45
Best Local Similarity 80.4%; Pred. No. 1.1e-103;
Matches 344; Conservative 16; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          Zhao M., Song H., Li N., Peng Y., Han Z., Chen Z.; Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF212224; AAF87326.1; -. PIR; A38643; A38643.
HSSP; Q00554; 1B18.
GO; GO:0005524; F:ATP binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53806 MW; 3B2AC6A3FFAE9461 CRC64;
                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR011009; Kinase like.
InterPro; IPR00719; Prot kinase.
InterPro; IPR002209; Ser thr pkinase.
InterPro; IPR002209; Ser thr pkinase.
ProDom; PD000001; Prot Kinase; 1.
SWART; SM00220; S TKC; 1.
PR0SITE; PS00110; PROTEIN KINASE ATP; 1.
PROSITE; PS00109; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN KINASE_DOM; 1.
                                                                                                                                                                     Created)
  464 RITLKEALKHPFFYPLKK 481
                                                                                                                                                                01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                                 (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      453 AA;
                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Bone marrow,
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   318
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OC Buka

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RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Sheamen C.W., Schuler G.D.,
R. Klausner R.D., Collins F.S., Wagner L., Sheamen C.W., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetcow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
B. Diatchenko L., Marushina K., Farmer A.A., Rubin G.W., Hong L.,
Stapleton M., Soares M.B., Toshiyuki S., Carminci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carminci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Rhy Whiting M., Madan A., Young A.C., Shevohenko Y., Bouffard G.G.,
Rhy Krzywinski M.I., Skalaka U., Smailus D.E., Schnerch A., Schein J.E.,
A Jones S.J., Marra M.A.;
RT "Generation and inlitial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
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Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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GO; GO:0004674; F:ATP binding; IEA.
GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
GO; GO:0006468; P:protein anino acid phosphorylation; IEA.
InterPro; IPR011009; Kinase like.
InterPro; IPR00129; Prot kinase.
InterPro; IPR002219; Ser thr pkinase.
InterPro; IPR00224; Ser thr pkinase.
InterPro; IPR001245; Tyr pkinase.
InterPro; IPR001245; Tyr pkinase.
SMART; SM00219; FYKC; I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC079006; AAH79006.1; -.
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                                                                                                               Last sequence update)
Last annotation update)
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PROSITE; PS00108; PROTEIN_KINASE_ST; UNKNOWN_1.
301 AA
                                                                               Created)
                                                                   25-0CT_2004 (TrEMBLrel. 28, 25-0CT_2004 (TrEMBLrel. 28, 25-0CT_2004 (TrEMBLrel. 28, Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
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ATP-binding; Kinase; Transferase.
SEQUENCE 498 AA; 59956 MW; 0A87B74D78889B19 CRC64;
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ID CLK2 MOUSE
AC 035491;
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KRAINCEECH II. TISSUE-Mammary tumor;

KRAINCEECH II. TISSUE-Mammary tumor;

KRAINCEECH II. TISSUE-Mammary tumor;

KRAINCEECH II. TISSUE-MAMMED E. A., Grouse L.H., Derge J.G.,

KRAUSHOER R.D., Felngold E. A., Grouse L.H., Derge J.G.,

KRAUSHOER R.D., COllins F.S., Wagner I., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Jedan H., Moore T., Max S.I., Wang J., Hshe F.,

RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,

RA Diatchenko L., Wodin T.B., Toshiyuki S., Carninoi P., Frange C.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RACHARGE S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RACHARGE S., Worley D.M., Sodergen B.J., Lu X., Glibbs R.A.,

RACHARGE S., Worley A., Young A.C., Shevchenko Y., Bouffard G.G.,

Willialon D.K., Marra M., Young A.C., Shevchenko Y., Bouffard G.G.,

RACHARGE S.J., Marra M.A., Young A.C., Shevchenko Y., Bouffard G.G.,

RACHIGUEZ A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

KZZYWinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,

T. "Generation and initial analysis of more than 15,000 full-length human man mouse cDNA sequences.",

T. And mouse CDNA sequences.",
                                                 384
                                                                                                                                                                                                                                           324
                                                                                                                                                                                                                SSAGRYVRRRCKPLKEFMLCHDEEHEKLFDLVRRMLEYDPTQRITLDEALQHPFFDLLKK 444
                                                                                                                                                VKYNSKMKRDERTLKNTDIKVVDFGSATYDDEHHSTLVSTRHYRAPEVILALGWSQPCDV
                                                                                                                     WSIGCILIEYYLGFTVFQTHDSKEHLAMMERILGPIPQHMIQKTRKRKYFHHNQLDWDEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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GO; GO:0005634; C:nucleus; IDA.
GO; GO:0004713; F:protein-tyrosine kinase activity; IDA.
GO; GO:0046777; P:autophosphosphorylation; IDA.
GO; GO:0018108; P:peptidyl-tyrosine phosphorylation; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.;
Submitted (CTT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC015089, AAM15080.1; -.
HSSP; Q03656; 1HOW.
MGD; MGI:1098669; C1k2
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Last annotation update)
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ProDom; PD000001; Prot kinase; 1.
SMART; SM00220; S TKG; 1.
PROSITE; PS500107; PROTEIN KINASE ATP; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE_ST; UNKNOWN_1.
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19,
26,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  372 KYFHHNOLDWDEHSSAGRYVRRRCKPLKEFMLCHDEEHEKLFDLVRRMLEYDPTQRITLD 431
                                                                                                                     72
                                                                                                                                                                                                                                                            290 KPENILFVNSDYELTYNLEKKRDERSVKSTAVRVVDFGSATFDHEHHSTIVSTRHYRAPE
                                                                                                                                                                                                                                  73 RRSS-PKRKRNRHCSSHQSRSKSHRRKRSRSIEDDEEGHLICQSGDVLRARYEIVDTLGE
                                                                                                                                                                                                                                                                                                                                               132 GAFGKVVECIDHGMDGMHVAVKIVKNVGRYREAARSEIQVLEHLNSTDPNSVFRCVQMLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                              192 WFDHHGHVCIVFELLGLSTYDFIKENSFLPFQIDHIRQMAYQICQSINFLHHNKLTHTDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        312 VILALGWSQPCDVWSIGCILIEYYLGFTVFQTHDSKEHLAMMERILGPIPQHMIQKTRKR
                                                                                                                     SHYLEARSL --- NERDYRDRRYVDEY - RNDYCEGYVPRHYHRDIESGYRIHCSKSSVRS
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                                                                Gaps
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-!- SUBCELLUIAR LOCATION: Nuclear (By similarity).
-!- PTM: Autophosphorylates on all three types of residues.
-!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. Lammer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
21-0CT-2004 (Rel. 45, Last annotation update)
22-OCT-2004 (Rel. 45, Last annotation update)
23-OCT-2004 (Rel. 45, Last annotation update)
37, Last annotation kinase CLK2 (RC 2.7.1.37) (RC 2.7.1.112)
38-CLK2 (RC 2.7.1.37)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i- FUNCTION: Phosphorylates serine- and arginine-rich (SR) proteing the spliceosomal complex may be a constituent of a network regulatory mechanisms that enable SR proteins to control RNA splicing. Phosphorylates serines, threonines and tyrosines.
-i- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mu
                                                             9
        Length 498;
                                                             Indels
  59.6%; Score 1437; DB 2; 60.6%; Pred. No. 5.2e-81;
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                                                             69; Mismatches
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MEDLINE=97439710; PubMed=9307018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SR) protein kinases.";
Biochem. J. 326:693-700(1997).
Query Match
Best Local Similarity 60.6'
Matches 262; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    443
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FUNCTION
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                                                                                                                                                                                                                                                                                                                                                                                                                        SRRSS-PKRKRNRHCSSHQSRSKSHRRKRSRSIEDDEEGHLICQSGDVLRARYEIVDTLG 130
                                                                                                                                                                                                                                                                                                                                                                                                                                    EGAFGKVVECIDHGMDGMHVAVKIVKNVGRYREAARSEIQVLEHLNSTDPNSVFRCVQML 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EWPDHHGHVCIVFELLGLSTYDFIKENSFLPFQIDHIRQMAYQICQSINFLHHNKLTHTD 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EVILALGWSQPCDVWSIGCILIEYYLGFTVFQTHDSKEHLAMMERILGPIPQHMIQKTRK 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   350 EVILELGWSQPCDVWSIGCIIFEYYVGFTLFQTHDNREHLAMMERILGPVPSRMIRKTRK 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    371 RKYFHHNQLDWDEHSSAGRYVRRRCKPLKEFMLCHDEEHEKLFDLVRRMLEYDPTQRITL 430
                                                                                                                                                                                                                                                                                                                                                                            71
                                                                                                                                                                            PROBON, PROBOGO 15 TRCE, Kinase; 1.

SWART; SM00200; STRCE, 1.

SWART; SM00200; STRCE; 1.

PROSITE; PSO0100; PROTEIN_KINASE DOW; 1.

PROSITE; PS00108; PROTEIN_KINASE DOW; 1.

PROSITE; PS00108; PROTEIN_KINASE ST; 1.

ATP-binding; Nuclear protein; Phosphorylation;
Serine/threonine-protein kinase; Transferase; Tyrosine-protein kinase.

NP BIND 163 479 Protein kinase.

NP BIND 163 176 ATP (By similarity).

BINDING 192 192 ATP (By similarity).

ACT SITE 289 289 Proton acceptor (By similarity).

SEQÜENCE 499 AA; 59955 MW; 092946BA171C9ADD CRC64;
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Pred. No. 2e-80;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                      69; Mismatches
                                                                                                             MGD; MGI:1098669; Clk2.
InterPro; IPR011009; Kinase like.
InterPro; IPR00719; Prot Kinase.
InterPro; IPR008271; Ser_thr_pkin_AS.
InterPro; IPR008290; Ser_thr_pkin_ase.
Pfam; PF00069; Pkinase; I.
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                                                                                       EMBL; AF033564; AAB87508.1; -. HSSP; Q03656; 1HOW.
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TISSUE-Lung, and Ovary.

TISSUE-Lung, and Ovary.

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Riauser R.D., Collins F.S., Magner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Appkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heith F.,

Diatchenco L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahe, J., Helton E., Ketteman M., Madan A., Roufigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Brown A. M. M. A. M. M. M. A. M. M
specificity protein kinase CLK2 (EC 2.7.1.37) (EC 2.7.1.112) (CDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-97474796; PubMed-9331372; Winfield S.L., Taybehl N., Martin B.M., Ginns E.I., Sidransky E.; Winfield S.L., Taybehl N., Martin B.M., Ginns E.I., Sidransky E.; "Identification of three additional genes contiguous to the glucocerebrosidase locus on chromosome 1q21: implications for Gaucher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hanes J.J., der Kammer H., Klaudiny J.J., Scheit K.H.; "Characterization by CDNA cloning of two new human protein kinases. Evidence by sequence comparison of a new family of mammalian protein
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PubMed=14759258; DOI=10.1186/gb-2004-5-2-r8;
Hillman R.I., Green R.E., Brenner S.E.
Han unappreciated role for RNA surveillance.";
Genome Biol. 5:RESEARCH008.1-RESEARCH008.16(2004).
-!-FUNCTION: Phosphorylates serine and arguinne-rich (SR) proteins of the spliceosomal complex may be a constituent of a network of regulatory mechanisms that enable SR proteins to control RNA splicing. Phosphorylates serines, threonines and tyrosines (By similarity).
-!-CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
-!-CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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-!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT)
MEDLINE=95082033; Pubmed=7990150;
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IsoId=P49760-1; Sequence=Displayed;
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                                                              inase 2).
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A MEDINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Attachul S.F., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

RA Attachnic L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M. J. Usdin T.B., Toodhlyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toodhlyuki S., Carninci P., Prange C.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan R.J., Malek J.J., Hulyk S.W.,

RA Hohton E., Ketremen M., Sodergren E.J., Lu X., Gibbs R.A.,

Raden J., Helton E., Ketreman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA T. "Generation and initial analysis of more than 15,000 full-length human and mones of the control of
                                                                                                                                              DLKPENILFVNSDYELTYNLEKKRDERSVKSTAVRVVDFGSATFDHEHHSTIVSTRHYRA 349
                                                                                                                                                                                                                                                            370 KRKYFHHNQLDWDEHSSAGRYVRRRCKPLKEFMLCHDEEHEKLFDLVRRMLEYDPTQRIT 429
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                                                                                                    PRVILALGWSQPCDVWSIGCILIEYYLGFTVFQTHDSKEHLAMMERILGPIPQHMIQKTR
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Genetic and genomic tools for Xenopus research: The NIH Xenopus initiative.";
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GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:001668; P:protein amino acid phosphorylation; IEA.
InterPro; IPR011009; Kinase_like.
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Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
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Last annotation update)
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470 LGEALQHPFFARLR 483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dev. Dyn. 225:384-391(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sednences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q03656; 1HOW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clk2-prov protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IISSUE=Embryo;
                         290
                                                                                                    310
                                                                                                                                                                                350
                                                                                                                                                                                                                                                                                                                                                                                                                           430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q7ZY59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     130 GEGAFGKVVECIDHGMDGMHVAVKIVKNVGRYREAARSEIQVLEHLNSTDPNSVFRCVQM 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    230 FDWFDYHGHMCISFELLGLSTFDFLKDNNYLPYPIHQVRHWAFQLCQAVKFLHDNKLTHT 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7
IsoId=P49760-2; Sequence=VSP 004856, VSP 004857;
Note=Lacks the kinase domain. May be produced at very low levels due to a premature stop codon in the mRNA, leading to nonsense-mediated mRNA decay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SRRSSPK--RKRNRHCSSHQSRSKSHRRKRSRSIEDDEEGHLICQSGDVLRARYEIVDTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        190 LEWFDHHGHVCIVFELLGLSTYDFIKENSFLPFQIDHIRQMAYQICQSINFLHHNKLTHT
                                                                                                                                                           PTM: Autophosphorylates on all three types of residues. SIMILARITY: Belongs to the Ser/Thr protein kinase family. Lammer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18 SHYLEARS----LNERDYRDRRYVDEY-RNDYCEGYVPRHYHRDIESGYRIHCSKSSVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        œ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, L29218; AAA61482.1; -.
EMBL, L29216; AAA61481.1; -.
EMBL, AF022268; AAC51817.1; -.
EMBL, BC014667; AAH14067.1; -.
EMBL, BC053603; AAH53603.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 59.7
les 259; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; S53637; S53637.
PIR; S53638; S53638.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72
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65 CSKSSVRSRRSSPKRKRNRHCSSHQSRSKSHR-RKRSRSIEDDEEGHLICQSGDVLRARY 123
                                                                                                                                                                                                                                                        96 SRDDSYRSTRRKQKRRNRRTRSYSQSSSSRSRRAKSVEDDVEGHLIYHSGDWLQERY 155
                                                                                                                                                                                                                                                                               EIVDTLGEGAFGKVVECIDHGMDGMHVAVKIVKNVGRYREAARSEIQVLEHLNSTDPNSV 183
                                                                                                                                                                                                                                                                                                                           184 FRCVQMLEWFDHHGHVCIVFELLGLSTYDFIKENSFLPFQIDHIRQMAYQICQSINFLHH 243
                                                                                                                                                                                                                                                                                                                                                                         NKLTHTDLKPENILFVKSDYVVKYNSKMKRDERTLKNTDIKVVDFGSATYDDEHHSTLVS 303
                                                                                                                                                                                                                                                                                                                                                                                     276 NKLTHTDLKPENILFVSSDYELRYNMEKKRDERCVKSTDIRVVDFGSATFDHEHHSTIVS 335
                                                                                                                                                                                                                                                                                                                                                                                                                     TRHYRAPEVILALGWSQPCDVWSIGCILIEYYLGFTVFQTHDSKEHLAMMERILGPIPQH 363
                                                                                                                                                                                                                                                                                                                                                                                                                                 336 TRHYRABEVLLELGWNQPCDVWSVGCIIFEYYVGFTLFQTHDNREHLAMMERILGPIPSR 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MIQKTRKRKYFHHNQLDWDEHSSAGRYVRRRCKPLKEFMLCHDEEHEKLFDLVRRMLEYD 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50 ERSRSYEE------RSSDRRAY-DRRYCDSYRRNDYSRDRGDVYYETDYD--YK-H 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ze-rEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Dual specificity protein kinase CLK3 (EC 2.7.1.37) (EC 2.7.1.112) (CDC like kinase 3).
                                                                                                                                                                                                                                                                                                                                         216 HLCVQMFDWFDYHGHMCISFELLGLSTFDFLKENNYFPYPIHQVRHMALQLCQAMKFLHD
                                                                                                                                                                                     6 EASHSVEEDTHPSHYLEARSLNERDYRDRRYVDEY-RNDYCEGYVPRHYHRDIESGYRIH
                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
MEDLINE-95062013; PubMed-7990150;
Hanes J.J., der Kammer H., Klaudiny J.J., Scheit K.H.;
"Characterization by cloning of two new human protein kinases.
Evidence by sequence comparison of a new family of mammalian protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                               16;
                                                                                                                                        Length 491;
                                                                                                                                                               94; Indels
                                                                                                                 58994 MW; 20870CC599623D3F CRC64;
                                                                                                                                                                                                                                                ::
InterPro; IPR002719; Prot kinase.
InterPro; IPR02290; Ser thr pkinase.
InterPro; IPR082291; Ser thr pkinase.
InterPro; IPR08271; Ser thr pkinase.
InterPro; Prinase; 1.
ProDom; PD000001; Prot kinase; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00101; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE ST; UNKNOWN I.
ATP-binding; Kinase; Transferase.
                                                                                                                                         DB 2;
                                                                                                                                                   ; Pred. No. 1.3e-78; 68; Mismatches 94
                                                                                                                                  58.0%; Score 1398;
Best Local Similarity 59.5%; Pred. No. 1...
Matches 262; Conservative 68; Mismarcher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORMS 1 AND 3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |::|:|| ||:||:||
456 PSKRMTLAAALKHPFFNPLK 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PTQRITLDEALQHPFFDLLK 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Mol. Biol. 244:665-672(1994)
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P49761; Q9BRS3; Q9BUJ7;
01-OCT-1996 (Rel. 34, Created)
28-FEB-2003 (Rel. 41, Last sequ
05-JUL-2004 (Rel. 44, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
                                                                                                                  491 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=CLK3;
                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                               124
                                                                                                                                                                                                                                                                                                                                                                         244
                                                                                                                                                                                                                                                                                                                                                                                                                     304
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Remainer R.D., Colling E.M., Grouse L.M., Derge J.G., Schubar G.D., Altennia R.P., Colling E.M., Grouse L.M., Schubar G.M., Schubar G.D., Altennia R.P., Cordan H., Woore T., Was S.J., Mang J., Haish F., Ranger G.M., Altennia R.M., Granger G.M., Gharastan P.M., Mannala R.D., Malled F.M., Glanger E.B., Mannala R.D., Malled F.M., Granger R.B., Gracia A.M., Gay L.J., Mulk S.W., Ranger S.A., McDhear P.J., Markernan K.M., Malda A.M., Gay L.J., Mulk S.W., Ralby S.M., Granger B.J., Markernan K.M., Malda A.M., Gay L.J., Mulk S.W., Ralby S.M., Retheman P.J., Markernan K.M., Mada A.M., Gay L.J., Mulk S.W., Ralby S.M., Retheman W.M., Scherger B.J., Marker M.M., Gay L.J., Mulk S.W., Malk S.M., Gay L.J., Mulk S.W., Markernan K.M., Scherger B.J., Marker M.M., Gay L.J., Mulk S.W., Marker M.M., Gay L.J., Scherker M.M., Gay L.J., Mulk S.M., Marker M.M., Gay L.J., Mulk S.M., Marker M.M., Gay L.J., Mulk S.M., Gay L.J., Mulk S.M., Marker M.M., Gay L.J., Mulk S.M., Gay L.J., Mulk S.M., Marker M.M., Gay L.J., Mulk S.M., Gay L.J., Mulk S.M., Gay L.J., Mulk S.M., Marker M.M., Gay L.J., Mulk S.M., Gay L.J., Mul
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
NCBI_TaxID=10116;
            norvegicus (Rat)
         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠે
       R InterPro; IRRO02719; Prot kinase.

R InterPro; IPR008271; Ser_thr_pkin_AS.

R InterPro; IPR008271; Ser_thr_pkin_AS.

R InterPro; IPR008270; Ser_thr_pkin_AS.

R Probom; PR000601; Prot kinase; 1.

R PROSITE; PS001001; PROTEIN KINASE APP; 1.

DR RRART; SM00120; ENCTEIN KINASE APP; 1.

R PROSITE; PS001107; PROTEIN KINASE APP; 1.

DR PROSITE; PS001107; PROTEIN KINASE APP; 1.

RW Alternative splicing; ATP-binding; Nuclear protein; Phosphorylation; KW Serine/threonine-protein kinase; Transferase; Tyrosine-protein kinase.

FT DOMAIN 156 472 Protein kinase; Transferase; Tyrosine-protein kinase.

FT NP BIND 165 170 ATP (By similarity).

FT ACT SITE 283 283 Proton acceptor (By similarity).

FT ACT SITE 283 283 Proton acceptor (By similarity).

FT VARSFLIC 124 152 RSQQSSRRSSRSUEDDKEGHUVCR.GDML -> MRLWGTWV FFT (PROSE).

FT ACT SITE 100 ATP (BY SIMILARITY).

FT ACT SITE 100 ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HRRKSRERGPYRTRKHAHHCHK------RTRSCSSASSRSQQSSKRSSRSVED 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEBGHLICQSGDVLRARYEIVDTLGEGAFGKVVECIDHGMDGMHVAVKIVKNVGRYREAA 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HIROMAYQICQSINFLHHNKLTHTDLKPENILFVKSDYVVKYNSKMKRDERTLKNTDIKV 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RSEIQVLEHLNSTDPNSVFRCVQMLEWFDHHGHVCIVFELLGLSTYDFIKENSFLPFQID 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VDFGSATYDDEHHSTLVSTRHYRAPEVILALGWSQPCDVWSIGCILIEYYLGFTVFQTHD 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SKEHLAMMERILGPIPQHMIQKTRKRKYFHHNQLDWDEHSSAGRYVRRRCKPLKEFMLCH 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 14
CLK3 RAT
AC 063117;
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last amnotation update)
DE bual specificity protein kinase CLK3 (BC 2.7.1.37) (BC 2.7.1.112) (CDC GN Name=CLK3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PPRRSRSRSHDRLP-----YQRRYRERRDSDTYR---CEERSPSFGEDYYGPSRSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYHRDIESG-YRI----HCSKSSVRSRRSSPKRKRNRHCSSHQSRSKSHRRKRSRSIED
                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                         42;
                                                                                                                                                                                                                                                                                                                                                                                          54.8%; Score 1321; DB 1; Length 490; 55.3%; Pred. No. 7.6e-74;
                                                                                                                                                                                                                                                                                                                                                                                                        ; Pred. No. 7.6e-74;
60; Mismatches 101; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 PLEASHSVEEDTHPSHYLEARSLNERDYRDRRYVDEYRNDYCEGYVP-
                                                                                                                                                                                                                                                                                                             /Missing (In isoform 3).
/FTId=VSP 004860.
SS -> TG (in Ref. 1).
86A342ABB8AB24CA CRC64;
                                                                                                                                                                                                                                                                                   Missing (in isoform 2) /FIId=VSP 004859.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEEHEKLFDLVRRMLEYDPTORITLDEALOHPFF 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   439 SLEHVQLFDLMRRMLEFDPAQRITLAEALLHPFF
InterPro; IPR011009; Kinase like.
InterPro; IPR000719; Prot_kInase.
                                                                                                                                                                                                                                                                                                                                                            58588 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 251; Conservative
                                                                                                                                                                                                                                                                                                                180
                                                                                                                                                                                                                                                                                                                                              132 1
490 AA;
                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                158
                                                                                                                                                                                                                                                                                                                                           CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  139
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DR PRIS, X9431; CAMULE

DR PRIS, 270352; S70352.

DR PRIS, 270352; S70352.

DR PRIS, 270352; S70352.

DR RGD; 651259; CLR3.

DR InterPro; IPR001009; Kinase like.

DR InterPro; IPR00229; Ser_thr_pkinase.

DR InterPro; IPR00229; Ser_thr_pkinase.

DR Promon; PR00020; Frct kinase; 1.

DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.

DR PROSITE; PS00107; PROTEIN KINASE DOM; 1.

DR PROSITE; PS00108; PROTEIN KINASE DOM; 1.

DR PROSITE; PS00108; PROTEIN KINASE ST; 1.

KW ATP-binding; Nuclear protein; Phosphorylation; KW ATP-binding; Nuclear protein kinase.

DOMAIN 156 472 Protein kinase.

TANDERS ATP (By similarity).

162 170 ATP (By similarity).

183 AM; 72F754F6A64AB19A CRC64;

The Protein Research of the protein kinase.

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SEQUENCE FROM N.A.
STRAIN=Sprague-Dawley; TISSUE=Brain;
STRAIN=Sprague-Dawley; TISSUE=Brain;
STRAIN=Sprague-Dawley; TISSUE=Brain;
SEGLAT STRAINES S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        similarity).
-!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.
-!- SUBCELLULAR LOCATION: Nuclear (By similarity).
-!- PTM: Autophosphorylates on all three types of residues.
-!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. Lammer
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199 RLEINVLKKIKEKDKENKFLCVLMSDWFNFHGHMCIAFELLGKNTFEFLKENNFQPYPLP 258
                                                                                                      286 VDFGSATYDDEHHSTLVSTRHYRAPEVILALGWSQPCDVWSIGCILIEYYLGFTVFQTHD 345
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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Strausberg R.;
Strausberg R.;
Strausberg R.;
Strausberg R.;
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.

B. Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.

B. GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0006749; F:protein serine/threonine kinase activity; IEA.

GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.

R. GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

R. GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

InterPro; IPR01019; Frot kinase.

R. InterPro; IPR002290; Ser Ehr pkinase.

R. InterPro; IPR001245; Tyr pkinase.

R. InterPro; PR001245; Tyr pkinase.

R. Pfam; PF00069; Pkinase; I.
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Name=Clk3;
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Prodom; PD000001; Prot_Kinase; 1.

SMART; SM00210; Trc; 1.

SMART; SM00219; Tyrkc; 1.

PROSITE; PS00107; PROTEIN KINASE ATP; 1.

PROSITE; PS00108; PROTEIN KINASE DOW; 1.

PROSITE; PS00108; PROTEIN KINASE ET; UNKNOWN_1.

ATP-binding; Kinase; Traniferase.

SEQUENCE 490 AA; 58485 MW; 6B10CA96A64AB19A CRC64;
                                                                                                                                                                                                                      Query Match 54.6%; Score 1316; DB 2; Best Local Similarity 55.1%; Pred. No. 1.6e-73; Matches 250; Conservative 60; Mismatches 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 439 SLEHVQLFDLMRRMLEFDPAQRITLAEALLHPFF 472
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Perfect scoré:

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Minimum Maximum Maximum

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X57186 Nouse clk m
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BX936001 Gallus ga
BX929601 Gallus ga
L28222 Homo sapien
MS9287 Human prote
ARS31674 Sequence
BV179987 squan10751
AX534244 Sequence
AX59282 Sequence
AC026097 Homo sapi
AC022096 Homo sapi
BC00220 Mus muscu
CQ718110 Sequence
AX653308 Mus muscu
BC079006 Rattus no
BX31976 Gallus ga
AB056421 Macaca fa
CQ715616 Sequence
BC011549 Homo sapi
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1 (bases 1 to 2354)

Yan,C., Ye,J., Ketchum,K.A., Di Francesco,V. and Beasley,E.M.
Isolated human kinase proteins, nucleic acid molecules encoding human kinase proteins, and uses thereof
Patent: US 6455291_A 1 24-SEP-2002;
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/organism="unknown"
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Result No.

721 TGGCGTATCAGATCTGCCAGTCAATAATTTTTACATCATAATAAATTAACCCATACAG 780 781 ATCTGAAGCCTGAAAATTTTTGTGAAGTCTGACTATGTAGTCAAATAATATTTTT 840 781 ATCTGAAGCCTGAAAAATATTTTGTTGAAGTCTGACTATGTAGTCAAATATATTCTA 840 841 AAATGAAACGTGATGAACGCACACTGAAAAACACGAGTATCAAAGTTGTTGAAA 900 841 AAATGAAACGTGATGAACGCACACTGAAAAACACAGATTTCAAAGTTGTTGAAA 900 841 AAATGAAACGTGATGAACACACAGAAAACAAGATTACAAAGTTGTTGAAA 900 901 GTGCAACGTATGATGAACACACACAGTACTTTGGAGTATCCAAGAGTTGTAGACTTTGGAA 900 901 GTGCAACGTATGATGAACACACAGAACTTTGGTGTCTTACCAGAGCTC 960 91 GTGCAACGTATGATGAACATCACAGAACTTTGGTGTCTTACGAGCACTACAGAGCTC 960 91 GTGCAACGTATTGGTTGAACATCACTCAGACTTTGGAGCATAGGTTACAGATTGCA 1020 91 CCGAGGTCATTTGGCTTTAGGTTGGTCTTGAGATTTGAACATTACATAGAACACAATAGTAAAGAGACAC 1020 91 TTCTTATTAGAATATTACCTTGGTTTTCAAACAATAGTAAAGAGACAC 1020	TICTTATTGAATATTACTTGGTTTCACAGTCTTTCAGACTCATGATAGTAAAGAGCACC TGCCAATGATGAATATTAGGTCCTTGCACTCATGATAGTAAAGAGCACC TGCCAATGATGAATATTACTTTGGTTTCACAGTCTTTCAGACTCATCATCATCATCAGAAACAAGAA TGCCAATGATGATGTTTTCACCATATTAGGACCCATACCACATGATTCAGAAAACAAGAA AACGCAAGTATTTTCACCATAACCAGCTAGCTTGGGATGAACACAGTTCTGCTGGTAGAT ATGTTAGGAGGCTGCAAACCGTTGAAGGATTTATGCTTTGTCATGATGAAGAACATG ATGTTAGGAGGCTGCAAACCGTTGAAGGAATTTATGCTTTGTCATGATGAAGAACATG ATGTTAGGAGCCTGCAAACCGTTGAAGGAATTTATGCTTTGTCATGATGAAGAACATC AGAAACTGTTTGACCTGCTTCGAAGAATGTTAGAATATGATCCAAAAGAATTACCT AGAAACTGTTTGACCTGGTTCGAAGAATGTTAGAATATGATCCAAAAGAATTACCT AGAAACTGTTTGACCTGGTTCGAAGAATGTTAGAATATGATCCAAAAGAATTACCT AGAAACTGTTTGACCTGGTTCGAAGAATGTTAGAATATGATCCAAAAGAATTACCT		1561 AAATTAAAATTAATTTTTTTTTTTTTTTTTTTTTTTT
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121 ATTATCGGGACCGGAGATACGTATACGAATACGGAATGACTACTGCGAGGATATCT	T21 TGGGGTATCAGATCTGCCAGTCAATAATTTTTTACATCATAATAATTAAT
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Seguence 1 from Patent WO0216567.
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                                                     TTTTGTATCAATAGCATAATTAACTTGTTAAGCAAGTATGGTCTTGATAATGCATTAGAA
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	661 CTTACGATTTCATTAAAGAAAACAGCTTTCTGCCATTTCAAATTGACCACATCAGGCAGA 720 721 TGGCGTATCACTCCCCAGTCATAAAATTTTTTACATAATAAATTAACCCATACAG 780 721 TGGCGTATCACTACAATAAATTTTTTACATCATAATAAATTAACCCATACAG 780	ATCTGAAGCCTGAAAATATTTGTTGAAGGTCTGACTATGTAGTAGTAGTAATTTTGTTGAAGTCTGACTATGTAGTAGTAATTTTTGTTGAAGTCTGACTATGTAGTAGTAGTAGTAGTAGTAGTAGTAGAGTCTGACTATGTAGTAGTATAATTTTGTTAGTAGAGTCTGACTATGTAGTCAAAAAATATTTGTTAGTAGTCTGACTATGTAGTCTGA	aratgrarcetgatgracgcacactgraraacacacgtatcargttgtgactttggra 	901 GTGCAACGTATGAACATCAAGTACTTTGGTGTACCCGACTTAAGAGCTC 960	961 CCGAGGTCATTTGGCTTTAGGTTTGGTCTCAGCCTTGTGATGTTTGGAGCATAGGTTGCA 1020 1021 TTCTTATTGAATATTACCTTGGTTTCACAGTCTTTCAGACTCATGATAGTAAGAGCACC 1080 1021 TTCTTATTGAATATTACCTTTGGTTTTCACATCTTTCAGACTCATGATAAGAGCACC 1080		1141 AACGCAAGTATTTTCACCATAACCAGCTACATTGGGATGAACACAGTTCTGCTGGTAGAT 1200 	1201 AIGITAGGAGACGCTGCAAACCGTTGAAGGAATTTAIGCTTTGTCAIGATGAAGAACAIG 1260 	1261 AGAAACHGTTTGACCTGGTTCGAAGAATGTTAGAATATGATCCAACTCAAAGAATTACCT 1320 	1321 TGGATGAAGCATTGCAGCATCCTTTCTTGACTTATTAAAAAGAAATGAAATTGGGAATC 1380 	1381 AGTGGTCTTACTATATACTTCTGGAAGAGATTACTTAAGACTGTGTCAGTCA	1441 CATTCTAATATTTTGTAAACATTAAATTATTTGTACAGTTAAATGTGTAAATATTGTAIG 1500 	1501 TITIGIALCAATAGCATAATTAACTTGTTAAGCAAGTATGGTCTTGATAATGCATTAGAA 1560 	1561 AAAITAAAAITAAITTICITTITGAAAITACCAITITIAAAIACCITIGAAAIAICCIT 1620 	1621 TGTGTCCAGTGATAAANGTGATTGATCTTGCCTTTTGTACATGGAGGTCACCTCTGAAGT 1680

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Db 1278 AGCTAGATTAGGATGAACACAGTTCTGCTGGTAGATATGTTAGGAGACGCTGCAAACCGT  Oy 1225 TGAAGGAATTTATGCTTTGTCATGATGAAGAACATGAGAAACTGTTTGACCTGGTTCGAA  Db 1338 TGAAGGAATTTATGCTTTGTCATGATGAAGAACATGAGAAACTGTTTGACCTGGTTCGAA  Oy 1285 GAATGTTAGAATATGATCCAACTCAAAGAAATACCTTGGATGAAGAACATTGCAGGCATCCTT  Db 1398 GAATGTTAGAATATGATCCAACTCAAAGAAATACCTTGGATGAAGAACATTGCAGCATCCTT  Oy 1345 TCTTGACTTATAAAAAAAGAAATGAAATGAGAATCAGTGGTTACTATAATACTTCTCT  Oy 1346 TCTTGACTTATAAAAAAAGAAATGAAATGAGAATCAGGATCATTATAATACTTCTCT  OY 1346 TCTTTGACTTATAAAAAAAAAAAAAAAATGAAATCATCATCTTATAATACTTCTTTATAAAAAAAA	1405 J 1405 J 1518 J 1465 J	OY 1525 TIGITAAGCAAGTATGGTCTTGATAATGCATTAGAAAATTAAAATTTTTTTT	Qy         1645 ATCTIGCCTTTTGTACATGGAGGTCACCTCTGAAGTGATTTTTTTT	1765 1878 1825	1885 1998 1945	2005 2005 2118 2005	Db 2178 AGATATAAAATTAGATAGAGAGGTTTCAGTTTTTAATACCAAGTCCTTAGGAG Qy 2125 TCTTAACATTGGCCAGCATCTTTATCAAATGACATAAATACGTAAACCTATAAGAATT 	OY 2185 AAGTTTATTAATTAGCCAATTTATGCTGTGATAATTCTTACGGGAGAAAGGGATTTGA
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JOURNAL Patent: WO 0073469-A 54 07-DEC-2000; Sugen, Inc. (US) FEATURES Location/Qualifiers 12488 /organism="Homo sapiens" /mol_type="unassigned DNA"	_xref="taxon:9606"	Query Match 87.0%; Score 2048; DB 6; Length 2488; Best Local Similarity 95.9%; Pred. No. 0; Matches 2148; Conservative 0; Mismatches 1; Indels 90; Gaps		Qy 145 ACGAATACAGGAATGACTACTGTGAAGGATATGTTCCTAGACATTATCACAGAGACATTG 20 	Qy 205 AAAGCGGGTATCGAATCCACTGCAGTAAATCTTCAGTCCGCAGCAGAGAAGCAGTCCTA 26	265 AAAGGAAGCGCAATAGACACTGTTCAAGTCATCAGTCACGTTCGAAGAGCACCGGAAGA 	QY 325 AAAGATCCAGGAGTATAGAGGATGATGAGGGGTCACCTGATCTGTCAAAGTGGAGACG 38	Oy 385 TTCTAAGAGCAAGATATGAAATCGTGGACACTTTGGGAGCCTTTGGCAAAGTTG 44	Qy 445.Tagagggattgatgatgggatgggatgggatggatggaggggaaaatggaaaaatg 50 	Qy 505 TAGGCCGTTACCGTGAAGCAGCTCGTTCAGAAATCCAAGTATTAGAGCACTTAAATAGTA 56 	Oy 565 CTGATCCCAATAGTGTCTTCCGATGTGTCCAGATGGTATGATCATCATGATC 62	Qy 625 AIGTITGTATIGTGTITGAACTACTGGGACTTAGTACTTACGATITCATTAAAGAAAACA 68	Oy 685 GCTTTCTGCCATTTCAAATTGACCACATCAGGCAGATGGCGTATCAGATCTGCCAGTCAA 74	OY 745 TAAATTTTTACATCATAATAAATTAACCCATACAGATCTGAAGCCTGAAAATATTTGT 80	OY 805 TIGIGAAGICTGACTAIGIAGICAAATATAATITCTAAAATGAAACGIGAIGAACGCACAC 86	Oy 865 TGAAAAACACAGATATCAAAGTTGTTGACTTTGGAAGTGCAACGTATGATGAACATC 92 
1578 AAATTAFTTTGTACAGTTAAGTGTAAATATTGTATGTTTTGTATCAATAGCATAATTAAC 1525 TTGTTAAGCAAGTATGGTCTTGATAATGCATTAGAAAATTAAATTAAATTTTTTTT	Qy 1585 GAAATTACCATTTTAAATACCTTTGAAATATCCTTTGTGTCCAGTGATAAATGTGATTG 1644	Qy         1645 AICTIGCCTTTTGTACATGGAGGTCACCTCTGAAGTGATTTTTTTGAGTAAAAGGAAAT         1704           Db         1758 AICTIGCCTTTTGTACATGAGGTCACCTCTGAAGTGATTTTTTTT	1705 CTTGACTATATATTCTTAAAGGAATATTCTTAATATCTTCAATTTAGAACTTAAC 		1825 GGTACTAGAAACCGAAAACTCAGAAATGTTTACTGTTAGAATTCTATTAAATTTTAAGTG 1938 GGTACTAGAAACCAAAACCAAAATGTTTACTGTTAGAATTCTATTAAAGTG		Qy         1945 CAGTITGTCCATTGTGTGACAGTTTGTTTAATAAAACCACACACA		Qy         2065 AGATATAAAAATAGAAATTCTGATGAGTTTTCAGTTTTTAATACCAAGTCCTTAGGAG 2124           Db         2178 AGATATAAAAATAGAAATTCTGATGAAAGGTTTCAGTTTTTAATACCAAGTCCTTAGGAG 2237		Qy         2185 AAGTTTATTAATTAATGTCTGTGATAATTCTTACGGGAGAAAGAGGATTTGA         2244           Db         2298 AAGTTTAATTAAGGCAATTTATGTCTGTGATAATTCTTACGGGAGAAAGAGGAATTTGA         2357	2245 TTGGAAAGCAGTTTGGGAAGAAAGTGCTGGAATTTCCAGAATTTAATTGGTTA 2358 TTGGAAAGAAGTTTGGAAGAAAAGTGCTGCTGAAATTTCCAGAATTTAATTGATTG	2305 CATAAACTITITGACTICAGAAAAAAA 2333 [11	SULT 7	LOCUS DEFINITION Sequence 54 from Patent WO0073469. ACCESSION AX056410 AVERSION AX056410 AVERSION AX056410	S

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Homo sapiens
Eukaryois Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Caterrhini; Hominidae; Homo.
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Plowman,G.D., Martinez,R., Whyte,D. and Sudersanam,S. Protein kinases

REFERENCE AUTHORS TITLE

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	RESULT 8 AF294429 AF294429 LOCUS DEFINITION Homo sapiens protein serine threonine kinase C1k4 mRNA, complete Cds. ACCESSION AF294429 VERSION KEYWORDS SOURCE Homo sapiens (human) ORGANISM Homo sapiens (human) AMARADORA; Momenalla; Entheria; Primates; Carariata; Wertebrata; Buteleostomi; Amanalla; Entheria; Primates; Cararihini; Hominidae; Homo.	KEFEKENCE  AUTHORS Schultz, J. Jones, T., Bork, P., Sheer, D., Blencke, S., Steyrer, S., AUTHORS Schultz, J., Jones, T., Bork, P., Sheer, D., Blencke, S., Steyrer, S., Wellbrock, U., Bevec, D., Ullrich, A. and Wallasch, C.  TITLE Molecular characterization of a cDNA encoding functional human CLK4 kinase and localization to chromosome 5q35 [correction of 4q35] JOURNAL Genomics 71 (3), 368-370 (2001)  WEDLINE 21100912 PUBMED 11170754 REFERENCE 2 (bases 1 to 1814) AUTHORS Schulz, J., Jones, T., Bork, P., Sheer, D., Blencke, S., Steyrer, S., TITLE HILLS HILLSCOK, U., Bevec, D., Ullrich, A. and Wallasch, C.	AL s urce	/ DE XTEEF = G1:9963396"  / DE XTEEF = G1:9963396"  / LTAIN 11 LOLD = WRHSKETHCPDWDSRESWGHESYRGSHKRKRRSHSSTQENRHCK PHOPKESDCHYLEARSINERDYRDKRYUDGYRNDYCEGYVPRHYHRD ESGYR.HGS RESYNBSRESSPKRKRHNGSSHQSRSKSHRRKSRSIEDDEEGHLICQSGDVLRARYE  KSSYNBSRESSPKRKRHCSHQSRSKSHRRKSRSIEDDEEGHLICQSGDVLRARYE  KDYLLGGARGKVVELDHGMDGHJAVKIVKNGYRRARSEIGVLEHINSTDPNS VFRCVQMLEWFDHGHVCIVFELLGLSTYDFIKENSFLPFOIDHIRQMAYQICQSINF  LHHNKLTHPIXDFPRILLFVKSDVYKYNSKMKRDEFLLKVYDFGSATYDDEHH STLVSTRHYRAPFVILALGWSQPCDVWSIGCILIEYYLGFTVFOTHDSKEHLAMWERI LGPIPQHMIQKTRKRYFHHNQLDWBEHSSAGRYVRRRCKPLKEFMLCHDESHEKLFD  LVRRMLEYDPTQRITLDEALQHPFPDLLKKK"  Query Match  69.3%; Score 1632; DB 9; Length 1814;  Best Local Similarity 99.3%; Pred. No. 3e-290;  Matches 1638; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
985 GGTCTCAGCCTTGTGATGTTTTGGAGCATAGGTTGCATTCTTATTGAATATTACCTTGGTT 1044  1148 GGTCTCAGCCTTGTGATGTTTTGGAGCATAGGTTGCATTCTTATTGAATATTACCTTGGTT 1207  1045 TCACAGTCTTTCAGACTCATGATAAAGAGCACCTGGCAATGATGAACTATTAG 1104  1208 TCACAGTCTTTCAGACTCATGATAAAGAGCACCTGGCAATGATGAAGAATATTAG 1267  1105 GACCCATACCACACACATGATTCAGAAACAGAACACAGAATTTTCACCATAACC 1164  1106 GACCCATACCACACACACACACACACACACACACACACAC	48 GAATCTTAGAATATCAACCAACTCAAAGAATTACCTTGGATGAAGCATTGCAGCATCCTT 48 GAATCTTAGAATATCATCCAACTCAAAGAATTACCTTGGAGAGCATTGCAGCATCCTT 345 TCTTTGACTTATTAAAAAGAAATGAAATGGGAATCAGTGGTCTTACTATATATCTTCT 508 TCTTTGACTTATTAAAAAGAAATGAAATGAAATGAATCAGTGGTCTTACTATATACTTCTCT 405 AGAAGAGATTACTTAAGACTGTGTCAACTAAACATTTTTTTT	1465 AAATTATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT		

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Strausberg, R.L., Feingold, B.A., Grouse, L.H., Derge, J.G., Schamen, C.M., Schuler, G.D., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Uddin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
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                                                                                                                                                                                                                                                                                                                                          WIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Contact: MGC help desk
Tissue procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
CDNA. Library Preparation: CLONTECH Laboratories, Inc.
CDNA. Library Arrayed by: The I.M.A.GG.E. Consortium (LINL)
BNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAL Plate: 51 Row: a Column: 9
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 10190705. Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fylell, Brin Garland, Ran Guin, Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
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Pahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA" / /mol_type="mRNA" | /mol_type="mRNA" | /db_xref="taxon:9606" | /clone="IMAGE:30324121" | /tissue_type="Skin and meninges pool- skin, dura matter, pia matter, choroid plexus." | /clone lib="NIH MGC_186" | /lab_host="DH10B"
                                                                                                                                                                                                                                                            Submitted (02-DEC-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2209 TCATGGCATGGCATGCATGTAGCAGTGAAAATCGTAAAAATGTAGGCGTTACCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             George Yang, Scott Zuyderduyn, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Vector: pDNR-LIB"
                                                                                                                                                                                                    (bases 1 to 3492)
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Matches 1325; Conservative
                                                                                                                                                                                                                                              Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               info@bcgsc.bc.ca
                                                                                                                                                                                                                             Strausberg, R.
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ACGAATACAGGAATGACTACTGTGAAGGATATGTTCCTAGACATTATCACAGAGACATTG
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                    GTCATTATTTAGAAGCAAGGTCCTTGAATGAGCGAGATTATCGGGACCGGAGATACGTTG
                                                                                                                                            AAAGCGGGTATCGAATCCACTGCAGTAAATCTTCAGTCCGCAGCAGAAAAGCAGTCCTA
                                                                                                                                                                           AAAGCGGGTATCGAATCCACTGCAGTAAATCTTCAGTCCGCAGCAGGAGAAGCAGTCCTA
                                                                                                                                                                                                                 AAAGGAAGCGCAATAGACACTGTTCAAGTCATCAGTCACGTTCGAAGAGCCACCGAAGGA
                                                                                                                                                                                                                                                                                      AAAGATCCAGGAGTATAGAGGATGAGGAGGTCACCTGATCTGTCAAAGTGGAGGACG
                                                                                                                                                                                                                                                                                                                                                           TTCTAAGAGCAAGATATGAAATCGTGGACACTTTGGGTGAAGGAGCCTTTTGGCAAAGTTG
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GTCATTATTTAGAAGCAAGGTCCTTGAATGAGCGAGATTATCGGGACACGGAGATACGTTG
                                                                       ACGAATACAGGAATGACTACTGTGAAGGATATGTTCCTAGACATTATCACAGAGACATTG
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Submitted (02-JUJ-2003) Biological Chemistry and Molecular Pharmacology, Harvard Institute of Proteomics, 320 Charles St., Cambridge, MA 02141-2023, USA

This CDS clone is a part of a collection of human full-length expression clones generated by Harvard Institute of Proteomics. Bach CDS has been cloned by Harvard Institute of Proteomics. Cterminal tag). The CDS has been directionally cloned using BD In-Fusion(TM) cloning system between the Sall and HindIII sites of the PDNR-Dual vector. Additional sequences in the clone: 'ACC' safter Sall site and before 'ATG' to provide Kozak consensus sequence; 'GG' after last codon and before HindIII site to maintain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PHOGRESOCHYLEAGELNERDYRDRYNDEYRNDYCEGYVPRHYHRDIESGYRIHCS
KSSYRSRRSSESPRKKRNRHCSSHQSRSKSHRRKRSRSIEDDEGGHILGOSGDYLRARYE
IVDTLGEGGAPGKVVECIDHGMGGHVAVKIVKNVGRYREAARSEIQVLEHLNSTDPNS
VFRCYQMLENFDHHRYCIVPELLGLSTYDFTKENSFLPFQIDHIRQMAYQICQSINF
LHHNKLTHTDLKPENILFVKSDYVVKXNSKWRDERTLKNTDIKVDFGSATYDDEH
STLOSTRYRAABVILALGGGORDOWSIGCILIEYYLGFTVRQTHOSKBHLAMMERI
LGPIPQHMIQKTRKRYFHHNQLDWDEHSSAGRYVRRRKCKFLKEFMLCHDEEHEKLEF
LVRRMLEYDPTQRITLDEALQHFFDLLKKKL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein id="AAQ02553.1"
/db_xref="GI:33304091"
/translation="MRHSKRTHCPDWDSRESWGHESYRGSHKRKRRSHSSTQENRHCK
                                                                                       AY335726 1446 bp mRNA linear SYN 15-OCT-2003 Synthetic construct Homo sapiens CDC-like kinase 4 (CLK4) mRNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="synthetic construct"
/mol type="mRNA"
/db_ref="taxon:32630"
/clone="Fthf000244.01L"
/tissue_type="placenta and brain"
/clone lib="First strand cDNA from placenta and brain"
/lab_host="DHSalpha T1 resistant"
/note="Vector: pDNR-Dual"
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synthetic construct
other sequences; artificial sequences.
1 (bases 1.01446)
Park, J., Rolfs, A., Hu, Y., Shen, B., Vannberg, F., Moreira, D.,
Kelley, T., Zuo, D., Raphael, J., Baqui, M., Jepson, D., Harlow, E.
                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 1446)
Park, J., Rollfs, A., Hu, Y., Shen, B., Vannberg, F., Moreira, D.,
Kelley, T., Zuo, D., Raphael, J., Baqui, M., Jepson, D., Harlow, E.
LaBaer, J. and Brizuela, L.
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Best Local Similarity 100.0%; Pred. No. 3.2e-226;
Matches 1284; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                        Cloning of human full-length CDS FLEXGene kinases in
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|gene="CLK4"
|note="Mutations: Stop->Leu"
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Unpublished
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AY335726
AY335726.1 GI:33304090
3469 AAAAAAAAAAAAAA 3484
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/gene="CLK4"
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DEFINITION
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AUTHORS
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IVDTLGEGAFGKVVECIDHGMDĞLAVAKIVKNVGRYREAARSEIQVLEHLNSTDPNS
YEKVÇMLEKREDHGHVCIVPELLGLEYYDERKENSFLPFQIDHIRQMAYQICOŞINF
LHHNKLTHTDLKPENILFYKSEYNYKKNSKRKRDERTLKNTDIKVUDFGSATYDDEHH
STLVSTRHYRAPEVILALGWSQPCDVWSIGCILIEYYLGFTVFQTHDSKEHLAMMERI
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LVRRMLEYDPARR I TLDEALQHPFFDLLKRK"
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KSSVRSRRSSPKRKRNRPCASHOSHSKSHRRKRSRSIEDDEEGHLICQSGDVLRARYB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MRHSKRTHCPDWDSRESWGHESYSGSHKRKRRSHSSTQENRHCK
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Series: IRAK Plate: 18 Row: c Column: 18
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 6671765.
Location/Qualifiers
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                                                                                                                                                                                                                                                                               /tissue_type="Mammary tumor metastatized to lung. Tumor arose spontaneously from a senescent normal mammary (clonal) outgrowth infected with the virus MMTV." (clone lib="MOI CGAP_Lu29" lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           505 TAGGCCGTTACCGTGAAGCAGCTCGTTCAGAAATCCAAGTATTAGAGCACTTAAATAGTA
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                                                                                                                                                                                                                          /db_xref="taxon:10090"
/clone="MGC:13871 IMAGE:3982920"
                                                                                                                                                                                                                                                                                                                                                                                                                       'note="Vector: pCMV-SPORT6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |db_xref="LocusID:12750"
|db_xref="MGI:1098551"
|c1="1546"
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Mus musculus CDC like kinase 4, mRNA (cDNA clone MGC:13871
IMAGE:1982920), complete cds.
                                                                                                                                                                                                                             1344
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                                                                                                                                                                                                                                                                                  1361 GAATGTTAGAATATGATCCAACTCAAAGAATTACCTTGGATGAAGCATTGCAGCATTGCTT 1420
  1165 AGCTAGATTGGGATGAACACAGTTCTGCTGGTAGATATGTTAGGAGACGCTGCAAACCGT 1224
                                                                                                                                                                  1301 rgaaggaarrrargcrrrgrcargargaagaacargagaacrgrrrgaccrggrrcgaa 1360
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Submitted (15-AUG-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
DNA Library Arrayed by: The I.M.A.G.B. Consortium (LINL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Pahey, Erin Helton, Mark Ketteman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
                                                                                                                                                                                                                          GAATGTTAGAATATGATCCAACTCAAAGAATTACCTTGGATGAAGGATTGCAGCATCCTT
                                      TGAAGGAATTTATGCTTTGTCATGAGGAACATGAGAAACTGTTTGACCTGGTTCGAA
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LOCUS
DEFINITION
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KEYWORDS
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AUTHORS
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/trainlation="MRHSKRTHCPDWDSRESWGHESYSGSHKRKRRSHSSTQENRHCK
PHOPKDSDCHYLEARCLMERDYRDRRYIDBYRNDYCEGYVPRHYHDDVSSTYRIHCS
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LVRRMLEYDPARRITLDEALQHPFFDLLKRR"
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                            Sugahara,T., Matsuda,A., Honda,G., Muramatsu,S. and Ishizawa,K. Stat6 activation gene Patent: WO 03104277-A 105 18-DEC-2003; Asahi Kasei Kabushiki Kaisha (JP)
                                  TTCTAAGAGCAAGATATGAAATCGTGGACACTTTGGGTGAAGGAGCCTTTGGCAAAGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTCATTATTTAGAAGCAAGGTCCTTGAATGAGGGAGATTATCGGGACCGGAGATACGTTG
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             TGATCTTGCCTTTTGTACATGGAGGTCACCTCTGAAGTGATTTTTTTGAGTAAAAGGAA
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Pred. No. 5.1e-225;
0; Mismatches 192;
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/note="unnamed protein product"
                                                                                                                                                                                              DNA
                                                                                                                                                                                              1881 bp DN from Patent WO03104277.
                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .1881
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="CAF06456.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                (house mouse)
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Oy 1525 TTGTTAAGCAAGTATGGTCTTGATAATGCATTAGAAAATTAAATTTTTTTT	RESULT 14 BD260616 LOCUS DEFINITION 49 human secreted proteins. ACCESSION BD260616 KEYWORDS UP 2002539776-A/16. SOURCE ORGANISM Homo sapiens (human) ORGANISM Extryoca, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Buteryota, Metazoa, Chordata, Catarrhini, Hominidae, Homo. AUTHORS ROBEN,C.A., Ruben, S.M. and Komatsoulis,G. TITLE TITLE JOURNAL Patent: JP 2002539776-A 16 26-NOV-2002;	HUMAN GENOME SCIENCES INC  COMMENT OB A HOMO SADJENB (human)  DN JD 2002539776-A/16  PN JD 2002539776-A/16  PD 26-NOV-2002  PP 16-MAR-1999 US 60/126051,10-DEC-1999 US 60/169906 PI CRAIG A ROSEN, STEVEN M RUBEN, GEORGE KOMATSOULIS PC CILINIS/09, AGIK35/36, AGIK38/00, AGIR48/00, AGIP17/02, AGIP25/14, PC AGIP25/16, PC AGIP25/18, AGIP25/24, AGIP25/28, AGIP29/00, CO7K14/47, CO7K16/18, PC CILINI/19, CILINI/21,	source Location/Qua 11222 /organism="H /mol_type="g /db_xref="ta	Ouery Match 50.3%; Score 1185; DB 6; Length 1222;  Best Local Similarity 99.9%; Pred. No. 5.46-208;  Matches 1196; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  Qy 517 GTGAAGCACCTCGTTCGAAATCCAAGAGTATTAGAGCACTTAAATAGTACTCATAATA 576	Db 9 GIGAAGCAGCTCAAAATCCAAAATCCAACTTTAGAGCACTTAAATAGTACTGATCCCAATA 68  Qy 577 GIGICTICCGAIGITGICCAAAIGGCTAGAATGGTTTGATCATCATGATCATGTTTGATG	OY 637 IGTITGAACTACTGGGACTTAGTACTTACGAITTCAITAAAGAAAACAGCTITCTGCCAI 696
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                     1 (bases 1 to 1456)
Cocks.B.G., Stuart,S.G. and Seilhamer,J.J.
Compositions for the detection of blood cell and immunological response gene expression
Patent: US 6607879-A 699 19-AUG-2003;
Location/Qualifiers
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    .1456
/organism="unknown"
/mol_type="genomic DNA"

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Best Local Similarity 99.7%;
Matches 1191; Conservative (
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Search completed: March 16, 2005, 14:31:50 Job time : 10138.3 secs

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- nucleic search, using sw model OM nucleic

March 16, 2005, 01:13:38; Search time 1244.4 Seconds (without alignments) 11198.198 Million cell updates/sec Run on:

US-10-801-671-1 2354 Perfect score:

IDENTITY NUC Scoring table: Sequence:

Gapop 10.0 , Gapext 1.0

8780412 Total number of hits satisfying chosen parameters:

4390206 segs, 2959870667 residues

Searched:

seq length: 0 seq length: 200000000 Minimum DB E Maximum DB E

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N\_Geneseq\_16Dec04: Database

geneseqn1980s:\*

geneseqn2003cs:\*geneseqn2003ds:\*geneseqn2004as:\* geneseqn2003as:\* geneseqn2003bs:\* geneseqn2002as:\*geneseqn2002bs:\* genesegn1990s:\* genesegn2000s:\* genesegn2001as:\* geneseqn2001bs:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2004bs:

Aad32038 Human kin Aax89402 Human cel Aax89852 Human pro Ad129373 Human MAR Ad129373 Human MAR Ad26142 Human coly Ad26142 Human coly Ad26140 Human pol Ad126140 Human col Ad131373 Human sec Ad131373 Human col Ad26181 Muman kin Ad507812 Mouse pol Ad607810 Human pol Ad524718 PRO polyp Ad54718 PRO polyp Ad07813 Mouse pol Ad524718 PRO polyp Ad07813 Mouse polyp Description SUMMARIES AAD32038 AAX898402 AAX898402 AAX8984675 AAD129373 AAD126140 AAC31772 AAD077809 AAC320283 AAC320283 AAC36140 AAD326140 AAD32039 AD077812 AAD32039 AD077812 AAD32039 AD077812 AAD32039 AD077813 Query Match Length DB 2488 2488 1446 1865 1446 21234 1455 1834 1834 1834 2354 2025.8 2020.6 2048 2048 1629.4 1300.6 1277.4 1118.2 1118.2 1097 813.2 811.6 811.6 811.6 Score 111 111 112 113 114 116 118 119 Result

Ado07814 Mouse pol	Adg74696 Human kin	Adh58715 Human CDC	Abk84044 Human cDN	Adl24750 Intestina	Ade77073 Human cDN	Aaf21734 Human bre	Adl24751 Intestina	Aca63031 Human clk	Abl64388 Stomach c	Abn95692 Gene #219	Adq15173 Human can	Adq83230 Human tum	Adg83910 Human tum	Adg84393 Human tum	Adq85141 Human tum	Adq86323 Human tum	Aad57339 Human kin	Aah46906 cDNA enco	Aas87541 DNA encod	Ado07807 Human pol	Adj62819 Human cDN	Ado07811 Mouse pol	Aac81771 Human bea	Acc46217 Human dit
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768.4	669.2	644.4	643.2	643.2	640.6	640	630.6	499.6	499.6	499.6	499.6	499.6	499.6	499.6	499.6	499.6	499.6	464.4	464.4	461.6	458.6	452.2	443	441.4
21	22	23	24	25	26	27	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

BP. AAD32038 standard; cDNA; 2354 (first entry) Human kinase protein cDNA. 18-JUN-2002 AAD32038; AAD32038 RESULT 1 

Human, kinase protein; enzyme; cytostatic; osteopathic; gene expression; colon-moderately differentiated adenocarcinoma; chromosome mapping; gene; drug screening; therapeutic; gene therapy; tissue typing; chromosome 5; bone osteosarcoma; ss. Homo sapiens

/\*tag= a 33. .1370 /\*tag= b /product= "Human kinase protein" 1371. .2354 /\*tag= c Location/Qualifiers Key S'UTR 3' UTR CDS

WO200216567-A2

28-FEB-2002.

24-AUG-2001; 2001WO-US026389.

24-AUG-2000; 2000US-0227470P. 19-MAR-2001; 2001US-00810671.

(APPL-) APPLERA CORP.

Beasley EM; Di Francesco V, Ye J, Ketchum KA, an C,

WPI; 2002-269354/31. P-PSDB; AAE20170.

New human kinase proteins and nucleic acids, useful in drug screening

assays, identifying modulators of kinase activity or treating c characterized by absence or unwanted expression of the protein.

Claim 4; Fig 1; 81pp; English

The invention relates to isolated human kinase proteins and nucleic acids. The nucleic acid and peptide sequences can be used as models for the development of human therapeutic targets, aid in the identification of therapeutic proteins and serve as targets for the development of human cof therapeutic agents that modulate kinase activity in cells and tissues that express the kinase. The nucleic acids are useful as probes or primers, in constructing recombinant vectors, for expressing antigenic portions of the proteins, chromosome mapping, drug screening, testing an containing cells that are aberrant in kinase gene expression. The proteins may be used in drug screening assays, in the identification of compounds that mall are aberrant in kinase gene expression. The proteins may be used in drug screening assays, in the identification of compounds that canalysis, in treating disorders characterised by an absence or unwanted analysis, in treating disorders characterised by an absence or unwanted canalysis, in treating disorders characterised by an absence or unwanted differentiated adenocarcinoma), and in generating antibodies specific for the peptides. Such antibodies can be used to detect the protein in situ, in vitro, or in cell lysate or supernatant, to isolate and purify the protein from host cells, pharmacogenomic analysis, tissue typing, and in this ting protein function. The present sequence is human protein cDNA. Human kinase protein gene is located on chromosome 5 

Sequence 2354 BP; 783 A; 370 C; 472 G; 729 T; 0 U; 0 Other;

240 360 540 540 900 600 TAGAATGGTTTGATCATCATGTCATGTTTGTATTGTGTTTTGAACTACTGGGACTTAGTA 660 120 180 240 300 300 360 420 420 480 480 CTGTTGAAGAGGACACTCATCCCAGTCATTATTAGAAGCAAGGTCCTTGAATGAGCGAG 120 121 ATTATCGGGACCGGAGATACGTTGACGAATACAGGAATGACTACTGTGAAGGATATGTTC 180 9 9 CTAGACATTATCACAGAGACATTGAAAGCGGGTATCGAATCCACTGCAGTAAATCTTCAG CACGITCGAAGAGCCACCGAAGGAAAAGAICCAGGAGIAIAGAGGAIGAIGAGGAGGGIC 361 ACCTGATCTGTCAAAGTGGAGACGTTCTAAGAGCAAGATATGAAATCGTGGACACTTTGG GTGAAGGAGCCTTTGGCAAAGTTGTAGAGTGCATTGATCATGGCATGGCATGCCATG TAGCAGTGAAAATCGTAAAAATGTAGGCCGTTACCGTGAAGCAGCTCGTTCAGAAATCC CTAGACATTATCACAGAGACATTGAAAGCGGGTATCGAATCCACTGCAGTAAATCTTCAG TCCGCAGCAGCAGCAGTCCTAAAAGGAAGCGCAATAGACACTGTTCAAGTCATCAGT ACCTGATCTGTCAAAGTGGAGACGTTCTAAGAGCAAGATATGAAATCGTGGACACTTTGG TAGCAGTGAAAATCGTAAAAAATGTAGCCGTTACCGTGAAGCAGCTCGTTCAGAAATCC AAGTATTAGAGCACTTAAATAGTACTGATCCCAATAGTGTCTTCCGATGTGTCCAGATGC AAGTATTAGAGCACTTAAATAGTACTGATCCCAATAGTGTCTTCCGATGTGTCCAGATGC 1 GCCAGCTGGGGTTACTTTAAAAAACATGCTCCATGTGCATCCCTCTTGAAGCTTCGCACT TCCGCAGCAGGAGAAGCAGTCCTAAAAGGAAGCGCAATAGACACTGTTCAAGTCATCAGT CACGTTCGAAGAGCCACCGAAGGAAAAGATCCAGGAGTATAGAGGATGATGAGGAGGTC GCCAGCTGGGGGTTACTTTAAAAACATGCTCCATGTGCATCCCTCTTGAAGCTTCGCACT Gaps ö Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTCATTATTTAGAAGCAAGGTCCTTGAATGAGCGAGATTATCGGGACCGGAGATACGTTG
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New cell cycle-regulating protein 53 and its polynucleotide, applice in diagnosis and treatment of malignant tumor, hemopathy, human immundeficiency virus infection, immunological diseases and various
                                                                                                                                                                                                                                                                                                                                                                        DB 4; Length 2497;
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                                                                                                                                                                                                                                                                                                                                                                        94.1%; Score 2215.8;
99.7%; Pred. No. 0;
iive 0; Mismatches
                                                                                                               Claim 6; Page 22-23; 30pp; Chinese.
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                                                                                                                                                               2371 AAGTTTATTAATTTAGGGAATTTATGTCTGTGATAATTCTTACGGGAGAAAGAGATTTGA
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                                                CAGTTTGTCCATTGTGACAGTTTGTTTAATAAAACCACATACACACTTTATTAAAGATTA
                                                                                                                                                                                                                                                           2311 TCTTAACATTGGCCAGCATCTGTTTATCAAATGACATAAATACGTAAACCTATAAGAATT
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                                                                                                 AAATCTAACTGGAAAGTCAGCTTGGAAAATGGACATTTCCAAGTATGTTTGGTGAGTCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human protein kinase (HPKM)-3 encoding nucleotide (clone ID 339963).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Corley NC;
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phosphate group; cancer; immune disorder; ss.
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128. .1483
/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                384
polypeptides respectively. The HPKM polypeptides can be produced recombinantly by standard recombinant methodology. Protein kinases add phosphate groups to proteins. HPKM polypeptide or an HPKM antagonist is used to treat or prevent cancer or an immune disorder. The present sequence represents the nucleotide sequence of HPKM-3
                                                                                                                                                                                              GTCATTATTTAGAAGCAAGGTCCTTGAATGAGCGGAGATTATCGGGACCGGAGATGTTG
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                                                                                                                                                                            GTCATTATTTAGAAGCAAGGTCCTTGAATGAGCGAGATTATCGGGACCGGAGATACGTTG
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                                                                                             Sequence 2446 BP; 788 A; 391 C; 516 G; 751 T; 0 U; 0 Other;
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Pred. No. 0;
0; Mismatches
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                                                                                                            2298 AAGTTTATTAATTAGGCAATTTATGTCTGTGATAATTCTTACGGGAGAAAAGAGATTTGA 2357
                                                                                                                                                          Human, mouse, protein kinase, antiarthritic, antisclerotic, osteopathic, immunosuppressive, cardiant, renal; antiinflammatory, antiasthmatic, dermatological; antidabetic, antiinfertility, gene therapy, vaccine, immune disorder, cardiovascular disease, neurodegenerative disease; cancer; autoimmune disorder, stroke, inflammatory bowel disease, inflammatory pelvic disease; antilammatory pelvic disease;
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                                                                                                                                  TCTTAACATTGGCCAGCATCTGTTTATCAAATGACATAAATACGTAAAACCTATAAGAATT
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stress related disorders, chronic inflammatory bowel disease, chronic inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis, psoriasis, rhinitis, autoimmunity, diabetes, cancers and reproductive disorders
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                                                                                                                                                                                                                                                        90;
                                                                                                                                                                                                     DB 4; Length 2488;
                                                                                                                                                Sequence 2488 BP; 819 A; 400 C; 504 G; 764 T; 0 U; 1 Other;
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                                                                                                                                                                                                        Score 2048;
Pred. No. 0;
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Best Local Similarity 95.9%;
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The invention relates to a compound comprising a sequence comprising 8-80 base pairs (bp) targeted to a nucleic acid encoding MARK3 (MAPK) microtubule affinity-regulating kinaes 3), that specifically of MARK3, i.e. is an antisense oligonucleotide (AO). Also included are a composition comprising the compound and a carrier or dilumet, inhibiting the expression of MARK3 in cells or tissues, treating an animal having or suspected of having a disease or condition associated with MARK3 and suspected for an antisense compound. The antisense oligonucleotide is useful for preparing a composition for treating hyperproliferative disease. The present sequence is a MARK3 associated with marks and acreening for an antisense compound. The antisense oligonucleotide is useful for preparing a composition for treating hyperproliferative disease. The present sequence is a MARK3 associated cDNA included in the figures but not mentioned anywhere else in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New antisense compound targeted to a nucleic acid molecule encoding microtubule-affinity-regulating kinases (MARK3), useful for modulating expression of MARK3 or for treating cancer or Alzheimer's disease.
                              TCTTAACATTGGCCAGCATCTGTTTATCAAATGACATAAATACGTAAAACCTATAAAGAATT
                                                                                                           2348 AAGITIATTAATTAAGGCAATTTATGTCTGTGATAATTCTTACGGGAGAAGAGGATTTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; ss; antisense gene therapy; MARK3; MAP/microtubule affinity-regulating kinase 3; cs
Alzheimer's disease; neurodegenerative disorde; hyperproliferative disorde;
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P-PSDB; ADI29255.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a novel isolated nucleic acid and the PRO polypeptide encoded by it. A protein of the invention has antiiniflammatory, antiarthritic, antirheumatic, immunosuppressive, costeopathic, antidiabetic, dematological, antipsoriatic, antiallergic, antiasthmatic, hepatotropic, and respiratory activity. A polymoleotide of the invention may have a use in gene therapy. The PRO polypeptide, its agonist, antagonist, or antibody that specifically binds to the capping useful for treating an immune related disorder such as systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, it invenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an idiopathic inflammatory myopathy, Sjogran's syndrome, systemic sclerosis, and idiopathic inflammatory myopathy, slogran's syndrome, antoimmune chronic aflease, a demyelinating disease of the central or peripheral nervous system, idiopathic demyelinating polymeuropathy, dullain-Barre syndrome, contonic inflammatory demyelinating polymeuropathy, a hepatobiliary contonic inflammatory demyelinating polymeuropathy, defined the control character in the control char
                                                          2304
                                                                                                                    2467
2348 AAGTTTATTAATTAGGCAATTTATGTCTGTGATAATTCTTACGGGAGAAAGAGAGATTTGA 2407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    biliary cirrhosis, granulomacus hepatitis, sclerosing cholangitis, biliary cirrhosis, granulomacus hepatitis, sclerosing cholangitis, inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's disease, an autorimmune or immune-mediated skin disease, abullous skin disease, erythema multiforme, contact dermatitis, psoriasis, an allergic disease, asthma, allergic rhinitis, atopic dermatitis, food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New PRO polypeptides and polynucleotides, useful for treating e.g. erythematosus, rheumatoid arthritis, diabetes mellitus, immune-mediated renal disease, or demyelinating diseases of the central or peripheral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BB; gene; PRO; antiinflammatory; antiarthritic; antirheumatic;
immunosuppressive; osteopathic; antidiabetic; dermatological;
antipsoriatic; antiallergic; antiasthmatic; hepatotropic; respiratory;
                                                                                        Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Williams PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polypeptide encoding cDNA SEQ ID NO:1571.
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                                                                                                                                                                                                                                  CATAAACTTTTGACTTCA 2486
                                                                                                                                                                           CATAAACTTTTGACTTCA 2323
                                                                                                                                                                                                                                                                                                                                                                                  ADP24393 standard; cDNA; 1814 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-419628/39.
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hypersensitivity, urticaria, an immunologic disease of the lung, eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity pneumonitis, a transplantation associated disease, graft rejection or graft-versus-host disease. The present sequence encodes a PRO protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          161 GTCATTATTTAGAAGCAAGGTCCTTGAATGAGCGAGATTATCGGGACCGGAGATACGTTG
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Pred. No. 5.8e-312;
0; Mismatches 11;
                                                                                                                                                                                                                                     69.3%;
                                                                                                                                                                                                                                   Query Match 69.3
Best Local Similarity 99.3
Matches 1638; Conservative
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Ishizawa K;

Muramatsu S,

o, Honda

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and activator of transcription 6 activation (5TAT6). The protein is useful for the producing an antibody, which involves administering the protein or its epitope-bearing fragments to a non-human animal as an antigen. The nucleic acid is useful for diagnosing a disease or susceptibility to a disease related to expression or activity of the protein. A transformant expressing the protein is useful for screening compounds which inhibit or promote STATG activation. A transformant expressing the protein is useful for producing a pharmaceutical composition. Compositions, antibodies and antisense molecules are useful for the treating a disease associated with STATG activation such as
                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a purified protein promoting signal transducer
                                                                                                                                                                                                                                                                                    New signal transducer and activator of transcription 6 activation promoting purified protein, for diagnosing and treating disease associated with activation/inhibition of transcription factor e.g.
                                                                                                                                                                                                                                                                                                                                                                     claim 4; SEQ ID NO 107; 1368pp; English.
                                                                            06-JUN-2002; 2002US-0385912P.
26-DEC-2002; 2002JP-00377326.
27-DEC-2002; 2002JP-00377326.
15-MAY-2003; 2003JP-00137505.
16-MAY-2003; 2003US-0470836P.
                                 05-JUN-2003; 2003WO-JP007123
                                                                                                                                                                                                           Sugahara T, Matsuda A,
                                                                                                                                                                            (ASAH ) ASAHI KASEI KK
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                                                                                                                                                                                                                                                                                                                                        diabetes and cancer
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                                                                                                                                                                                                                                                               SRATG; immunogen; STATG activation; allergy; inflammation; autolimmunogen; STATG activation; allergy; inflammation; autolimmunogen; diabetes; hyperlipidaemia; infection; cancer; Thi hyperactive disease; rheumatoid arthritis; osteoarthritis; systemic lupus erythematosus; sepsis; asthma; allergic rhinitis; schaemic heart disease; subarachnoid haemorrhage; viral hepatitis; AIDS.
                                                                                                                                                                                                                  Human cDNA encoding protein that promotes STAT6 activation #54.
                                                                           ВЪ
                                                                      ADI26142 standard; cDNA; 1792
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22-APR-2004

ADI26142;

WO2003104277-A2 Homo sapiens

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allergic diseases, inflammation, autoimmune diseases, diabetes, hyperlipidaemia, inflammation, autoimmune diseases, diabetes, hyperlipidaemia, infections disease and cancers. Compositions are useful for treating disease ascordated with STATE activation and/or prevention of Thi hyperactive diseases. Compositions are also useful in rheumatoid altergic rhinitis, ischemic luques erythematosus, sepsis, asthma, allergic rhinitis, ischemic luques erythematosus, sepsis, asthma, viral hepatitis and AIDS. The protein has efficient promoting STATE activity. The protein or nucleic acid is effectively useful for screening compounds for treating and preventing disease associated with excessive activation or inhibition of STATE. The present sequence represents a human cDNA encoding a protein which promotes STATE activation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GICATTATTTAGAAGCAAGGTCCTTGAATGAGCGAGATTATCGGGACCGGAGATGTTG
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Oy 1465 AAATTATTTGTACAGTTAAGTGTAATTTGTATGTATCAATAGCATAATTAAC 1524	RESULT 8 AAC81772 ID AAC81772 standard; DNA; 1323 BP. XX AC AAC81772; XX AC AAC81772; XX DT 23-PEB-2001 (first entry)	XX DE Human beacon partial coding sequence SEQ ID NO: 7. XX XX XX XX XX YX YX YX YX YX YX YX YX	XX PR 23-APR-1999; 99AU-00009919. PR 24-MAR-2000; 2000AU-00006454. XX XX PA (AUTO-) AUTOGEN PTY LTD. XX		The present invention is relabeacon from the Israeli sand regulation of energy balance, analogues can be used in the energy imbalance, metabolic finsulin resistance. In additiproduce leaner animals  Sequence 1323 BP; 452 A; 199 Duery Match 55.3%;	Best Local Similarity 98.9%; Pred. No. 1.1e-246; Matches 1309; Conservative 0; Mismatches 14; Indels 0; Gaps 0;  Qy 697 TTCAAATTGACCACATCAGGCAGATGGCGTATCAGATCTGCCAGTCAATAAATTTTTAC 756
	685 GCTTTCTGCCATTTCAAATTGACCACATCAGGCAGATGGCGTATCAGATCTGCCAGTCAA 744		1001 ACAGHACTTTGGTGTCTACCGGCACTACAGAGCTCCGAGGTCATTTTGGCTTTTAGGTT 1060 985 GGTCTCAGCCTTGTGATGTTTGGAGCTTGCATTCTTATTGAATATTTGCTTTGGTT 1044	1181 GACCCATACCACACACATGATTCAGAAAACAAGAAACGCAAGTATTTCACCATAACC 1240 1165 AGCTAGATTCGGATGACTCTGCTGGTAGATATGTTAGGAGACGCTGCAAACCGT 1224 1167 AGCTAGATTCGGATGAACACAGTTCTGCTGGTAGATATGTTAGGAGACGCTGCAAACCGT 1224 1241 AGCTAGATTCGGATGAACACAGTTCTGCTAGATATGTTAGGAGACGCTGCAAACCGT 1300	1225 TGAAGGAATTTATGCTTTGTCATGAAGAACATGAGAACTGTTTGACCTGGTTCGAA 1284	agaagagattacttaagactgtgtgagtgagtaaagattctaatattttgtaaagatt 

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g compounds that influence cell that expresses a gene didentifying fat cell the agent. The method an agent, exposing the ession of the gene sion vector not exposed to lidentifying fat cell ses an antisense prefatably a human. The nd an agent, exposing the lihe agent to the alpoptide, treating a number or size in the hod of regulating fat cell ntaining fat cells and an in the laize or number in the
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AAGATTAAAATCTAACTGG 2016
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   1061 GGTCTCAGCCTTGTGATGTTTGGAGCATAGGTTGCATTCTTATTGAATATTACCTTGGTT 1120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ss; gene; human; signal transducer and activator of transcription 6; STAT6; immunogen; STAT6 activation; allergy; inflammation; autoimmune disease; diabetes; hyperlipidaemia; infection; cancer; Thl hyperactive disease; rheumatoid arthritis; osteoarthritis; systemic lupus erythematosus; asepsis; asthma; allergic rhinitis; ischaemic heart disease; subarachnoid haemorrhage; viral hepatitis; AIDS.
                                                                                                                  GACCCATACCACAACACATGATTCAGAAAACAAGAAAACGCAAGTATTTTCACCATAACC
                                                                                                                                                                           TGAAGGAATTTATGCTTTGTCATGAAGAACATGAGAACTGTTTGACCTGGTTCGAA
                                                                 TCACAGTCTTTCAGACTCATGATAGTAAAGAGCACCTGGCAATGATGAACGAATATTAG
                                                                                              GACCCATACCACACCCATGATTCAGAAAACAAGAAAACGCAAGTATTTTCACCATAACC
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06-JUN-2002; 2002JP-0317326.
27-DEC-2002; 2002JP-00317326.
27-DEC-2003; 2003JP-00137505.
15-MAY-2003; 2003JF-00137505.
16-MAY-2003; 2003JS-0470836P.
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subject is altered. The method is useful for identifying compounds the infiluence fat cell number or size, for preparing a composition for treating or preventing obesity or diabetes. This sequence represents human cDNA used in the scope of the invention.
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                                                                                                          54.6%; Score 1286; DB 12; Length 1446;
.larity 100.0%; Pred. No. 8.8e-244;
Conservative 0; Mismatches 0; Indels 0;
                                                                            Sequence 1446 BP; 474 A; 258 C; 332 G; 382 T; 0 U; 0 Other;
                                                                                                                        Best Local Similarity
Matches 1286; Conser
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The invention relates to a purified protein promoting signal transducer and activator of transcription 6 activation (STAT6). The protein is useful for the producing an antibody, which involves administering the protein or its epitope-bearing fragments to a non-human animal as an antigen. The muclaic acid is useful for diagnosing a disease or susceptibility to a disease related to expression or activity of the protein. A transformant expressing the protein is useful for screening compounds which inhibit or promote STAT6 activation. A transformant compounds which inhibit or promote STAT6 activation are useful composition. Compositions, antibodies and antisense molecules are useful composition. Compositions, antibodies and antisense molecules are useful for the treating a disease associated with STAT6 activation such as allergic diseases, inflammation, autoimmune diseases, diabetes, hyperlipidaemia, infections disease and cancers. Compositions are useful for treating disease associated with STAT6 activation and/or prevention of Th1 hyperactive diseases. Compositions are also useful in rheumatoid allergic rhinitis, ischaemic heart diseases, submarachnoid haemorrhage, viral hepatitis and AIDS. The protein has efficient promoting STAT6 activation or inhibition of STAT6. The present sequence represents a curivation or inhibition of STAT6. The present sequence represents a human cDNA encoding a protein which promotes STAT6 activation.
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Sequence 1881 BP: 570 A: 344 C; 450 G; 517 T; 0 U; 0 Other;

2,	144	309	369	264	429	324	489	384	549	444	609	504	699	564	729	624	789	684	849	744	606
ince 1881 BP; 570 A; 344 C; 450 G; 517 T; 0 U; 0 Other; tch 54.3%; Score 1277.4; DB 12; Length 1881; al Similarity 87.9%; Pred. No. 4.6e-242; Indels 3; Gaps. 1413; Conservative 0; Mismatches 192; Indels 3; Gaps.		250 GTCACTATTTAGAAGCAAGATGCTTGAATGAGAGATATTATCGGGACCGGAGATACATTG 145 ACGAATACAGGAATGACTGCTGAAGGATATGTTCCTAGACATTATCACAGAGACATTG		205 AAAGGGGGTATCGATCCACTGCAGTAAATCTTCAGTCCGCAGCAGAGAAGAGTCCTA	370 AAAGCACTTACCGGATCCATTGCAGTAAATCCTCAGTCAG	265 AAAGGAAGCGCAATAGACACTGTTCAAGTCATCAGTCACGTTCGAAGACCACCGAAGGA	430 AGAGAAAGCGTAATAGACCCTGTGCAAGTCATCAGTCGCATTCGAAGAGCCACCGAAGGA	325 AAAGATCCAGGAGTATAGAGGATGATGAGGAGGTCACCTGATCTGTCAAAGTGGAGAGG	490 AAGATCCAGGAGTATAGAGGATGATGAGGGGCTCACCTGATCTGTCAAAGTGGAGAGG	95 TICTAAGAGCAAGATATGAAATCGTGGACACTTTGGGTGAAGGAGCCTTTGGCAAAGTTG	50 TICTAAGAGCAAGATATGAAATCGTGGACACTTTAGGTGAAGGAGCCTTTGGCAAGTTG	45 TAGAGTGCATTGATCATGGCATGGATGGATGTAGCAGTGAAAAATG	610 TAGAGTGCATTGATCACGGCATGGATGGCTTACATGTAGCAGTGAAAATTGTAAAAATG	505 TAGGCCGTTACCGTGAAGCAGCTCGTTCAGAAATCCAAGTATTAGAGCACTTAAATAGTA	670 TAGGCCGTTACCGGGAGGCAGCTCGTTCTGAAATCCAAGTATTGGAGCACTTGAACAGCA	565 CTGATCCCAATAGTGTCTTCCGATGTGCTAGAAGGTTTGATCATCATCATGTC	730 CTGACCCCAACAGTGTCTTCCGATGCGTCCAGATGCTAGAGTGGTTTGATCATCATGGTC	625 AIGTITGIAITIGIGITIGAACIACIGGGACITAGIACITACGATITCAITAAAGAAAACA	790 ATGITITITITITITITITITITITITITITITITITITI	685 GCTTTCTGCCATTTCAAATTGACCACATCAGGCAGATGGCGTATCAGATCTGCCAGTCAA	850 dririciecearticaaartearcacarcaaareeerrarcaearere
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ATCATAATAAATTAACCCATACAGATCTGAAGCCTGAAAATATTTTGTTTTGTGAAGTCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to the isolation of genes AACS9277-CS9325 encoding 49 human secreted proteins AAB33718-B33764. The genes can be used to generate fusion proteins by linking to the gene for the human compared to immunoglobulin G FC portion (SEQIDI) for increasing the stability of the immunoglobulin G FC portion (SEQIDI) for increasing the stability of the fusion protein as compared to the human protein only. The genes and conditions, e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic a range of human tissues disclosed in the specification. The nucleic diagnosis, treatment and prevention of: (a) cancer, e.g. breast and covarian cancer, and other cancers of the adrenal gland, bone, bone cancers, gastroinestinal tract, liver, lung, or urogenital, (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, comultiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular diseases e.g. ecrebral anoxia and epilepsy; and (f) infectious diseases e.g. ecrebral anoxia and epilepsy; and (f) infections diseases e.g. ecrebral anoxia and epilepsy; and (f) infections diseases such as viral, fungal and parasitic (f)
                                       Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiuleer; vulnerary; anticonvulsant; antiacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein; ss.
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Pred. No. 6.9e-224;
0; Mismatches 0; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1222 BP; 407 A; 194 C; 229 G; 392 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acid molecules encoding human secreted preventing, treating or ameliorating a disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 349-350; 410pp; English.
Human secreted protein cDNA #7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50.3%;
                                                                                                                                                                                                                                                                                                                                                         99US-0126051P.
99US-0169906P.
                                                                                                                                                                                                                                                                                                                16-MAR-2000; 2000WO-US006765
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 99.5
Matches 1196, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rosen CA, Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-594570/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; AAB33724.
                                                                                                                                                                                                                       WO200056753-A1.
                                                                                                                                                                                                                                                                                                                                                            23-MAR-1999;
10-DEC-1999;
                                                                                                                                                                                                                                                                    28-SEP-2000
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A composition comprising a plurality of cDNAs, useful for detecting altered expression of genes in an immunological response or for diagnosing and treating an immunopathology, e.g. Crohn's disease, asthma
                 Human; gene; 88; immunological response; immunopathological condition; Crohn's disease; asthma; ulcerative colitis; hypereosinophilia; irritable bowel syndrome; osteoarthritis; rheumatoid arthritis; acute monocytic leukaemia; antiinflammatory; antiasthmatic; antiulcer; osteopathic; antiarthritic; antirheumatic; cytostatic.
                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 699; 50pp; English.
                                                                                                                                                                                    Seilhamer
                                                                                                                              98US-00023655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50.1%;
                                                                                                                                               98US-00023655
                                                                                                                                                                                    Stuart SG,
                                                                                                                                                                   CORP.
                                                                                                                                                                                                       WPI; 2003-895307/82.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                   or osteoarthritis.
Human cDNA #699
                                                                                                                                                                   (INCY-) INCYTE
                                                                                                                               19-FEB-1998;
                                                                         sapiens
                                                                                          US6607879-B1
                                                                                                             19-AUG-2003
                                                                                                                                                                                     Cocks BG,
                                                                          Homo
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The invention relates to a composition comprising a plurality of CDNAs for detecting the altered expression of genes in an immunological cresponse. The invention also relates to a method of diagnosing or monitoring the invention also relates to a method of diagnosing or monitoring the treatment of an immunopathological condition in a sample, comparising obtaining nuclaic acids from a sample, contacting the nuclaic acids of the sample with an array comprising the plurality of cDNAs under conditions to form one or more hybridisation complexes, detected to EDNAs under conditions to form one or more hybridisation complexes and recent leavel of the detected hybridisation complexes with the level of hybridisation complexes correlates with the presence of an immunopathological condition. Also disclosed are an expression profile comprising a microarray and a plurality of detectable complexes and a method for identifying a plurality of polynucleotide probes. The CDNAs are useful as hybridisable array elements in a microarray for monitoring the expression of target polynucleotides. The microarray for monitoring the expression of target polynucleotides. The microarray for monitoring the expression of the timmunopathology, such as Crohn's diseases, asthma, culcarative colitis, hypercosinophila, irritable bowel syndrome, carcinogenicity studies, forensics or pharmacogenomics. The composition may also be used in fluy discovery and development, toxicological and carcinogenicity studies, forensics or pharmacogenomic fragments. This sequence represents a human cDNA of the invention. Note: The sequence data for this patent did not form part of invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly formation. the printed specification but was obtained in from USPTO at segdata.uspto.gov/sequence.html.

Sequence 1456 BP; 480 A; 213 C; 261 G; 502 T; 0 U; 0 Other;

Query Match	atch	50.1%;	Score	1178.2;	DB 11;	50.1%; Score 1178.2; DB 11; Length 1456;	1456;		
Matches	best Local Similarity >9.7%; Fred. No. 1.06-222; Matches 1191; Conservative 0; Mismatches 3; Indels 1; Gaps	yy./*; tive	Fred. 0; Mis	39.78; Fred. No. 1.06-222; ive 0; Mismatches 3;	3;	Indels	1,	Gaps	1,
٥,	1003 TTTGGAGCATAGGTTGCATTCTTATTGAATATTACCTTGGTTTCACAGTCTTTCAGACTC 1062	GGTTGCAT	TCTTAT	RGAATATTA	CCTTGGI	TTCACAGT	TTTCA	GACTC	1062
<b>q</b> q	262 TGTAGCGCATAGGGTTGCATTCTTATTGAATATTACCTTGGGTTTCACAGTCTTTCAGACTC 321	GGTTGCAT	TCTTAT	rgaatatta	CCTTGGT	TTCACAGT	CTTTCA	GACTC	321
٥, م	1063 ATGATAGTAAAGAGCACCTGGCAATGATGGAACGAATATTAGGACCCATACCACAACACA 1122	GAGCACCT	GGCAATC	SATGGAACG	AATATTA	GGACCCATA	ACCACA	ACACA	1122
DP QD	322 ATGATAGTAAAGAGCACCTGGCAATGATGGAACGAATATTAGGACCCATACCACAACACA 381	GAGCACCT	GGCAATC	SATGGAACG	AATATTA	GGACCCATA	ACCACA	ACACA :	381

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1041 1841 1901 1161 1302 1422 1482 1542 1661 1721 1781 1961 1221 2021 1281 2081 1341 1601 1182 1101 441 501 561 621 681 741 801 861 921 981 TGATTCAGAAAACAAGAAACGCAAGTATTTTCACCATAACCAGCTAGATTGGGATGAAC TGATTCAGAAAACAAGAAAACGCAAGTATTTTCACCATAACCAGCTAGATTGGGATGAAC GTCATGATGAAGAACATGAAACTGTTTGACCTGGTTCGAAGAATGTTAGAATATGATC GTCATGAAGAACATGAGAAACTGTTTGACCTGGTTCGAAGAATGTTAGAATATGATC CTTAAAGGAATATTCTTTATATATACTTCAAATTTAGAACTTAACTTTAAAGTTTTTTCTTC TGTAATTGTTGAACGGGTGATTATTATTAACTCTAGATAAGCAGGTACTAGAAACCAAAA CTCAGAAAATGTTTACTGTTAGAATTCTATTAAATTTTTAAGTGTTGTATTCTTTTTCATT CTCAGAAAAIGTTTACTGTTAGAATTCTATTAAATTTTTAAGGTGTTGTATTCTTTTTCATT GGGTGATGTCAGGGTGATAACCAGACATTCATGGAAAGGCATGCAGTTTGTCCATTGTGA GGGTGATGTCAGGGTGATAACCAGACATTCATGGAAAGGCATGCAGTTTGTCCATTGTGA CAGITIGITIAATAAAACCACATACACCTTTTATTTAAGATTAAAATCTAACTGGAAAGT ACAGTTCTGCTGGTAGATATGTTAGGAGACGCTGCAAACCGTTGAAGGAATTTATGCTTT AGAAATGAAATGGGAATCAGTGTCTTACTATATACTTCTCTAGAAGAGATTACTTAAAGA CTGTGTCAGTCAACTATTCTAATATTTTTGTAAACATTAATTTTTTGTACAGTT <u>AAGTGTAAATATTGTATGTATCAATAGCATAATTAACTTGTTAAGCAAGTATGGT</u> 742 AAGTGTAAATATTGTATGTTTTGTATCAATAGCATAATTAACTTGTTAAGCAAGTATGGT TGGAGGTCACCTCTGAAGTGATTTTTTTTTTGAGTAAAAGGAAATCTTGACTACTTTATATT CTTAAAGGAATATTCTTTATATACTTCAAATTTAGAACTTAAACTTTAAAAGTTTTTTCTTC TGTAATTGTTGAACGGGTGATTATTAATTAACTCTAGATAAGCAGGTACTAGAAAACCAAAAA CAGTITGTITAAAAAACCACATACACACTITAATTAAGATTAAAATCTAACTGGAAAGT CAGCITGGAAAATGGACATTTCCAAGTATGTTTGGTGAGTCACAGATATAAAAATAGAAA TTCTGATGAGGGTTTTCAGTTTTTAATACCAAGTCCTTAGGAGTCTTAACATTGGCCAGC Trcreardadaderrrcagrrrraaraccaagrccrraggagrcrraacarrdgccagc 2196 **ATCTGTTTATCAAATGACATAAATACGTAAACCTATAAGAATTAAGTTTAAT** 1123 382 1363 682 1042 1102 1183 1243 1303 1423 1483 1543 1602 1662 1722 1782 1842 1902 1162 1962 1222 2022 1282 2082 1342 2142 442 502 562 622 802 862 922 982 g 셤 8 Š 셤 ò a ò g ઠે 요 8 셤 8 g Ś 요 8 엄 ò 셤 ò a ò 임 à 셤 ò à d à В

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Gaps ..

0; Mismatches 129; Indels

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compounds which inhibit or present or expression or activity of the spread or a disease related to expression or activity of the susceptibility to a disease related to expression or activity of the protein. A transformant expressing the protein is useful for screening compounds which inhibit or promotes TATAT activation. A transformant expressing the protein is useful for producing a pharmaceutical composition. Compositions is untibodies and antisense molecules are useful for the treating a disease associated with STATAT activation such as allergic diseases, inflammation, autoimmune diseases, diabetes, byperlipidaemia, inflammation, autoimmune diseases, diabetes, composition and/or prevention of Thi hyperactive diseases. Compositions are also useful in rhewmatoid arthritis, osteoarthritis, systemic lupus erythematosus, sepsis, asthma, allergic rhinitis, ischaemic heart diseases, subarachnoid haemorrhage, viral hepatitis and AIDS. The protein has efficient promoting STATE compounds for treating and preventing disease associated with excessive activation or inhibition of STATE. The present sequence represents a continuation.
                                                                                                                                                                                                                                                                                                                                                                   STATE; immunogen; STATE activation; allergy; inflammation; autoimmune disease; diabetes; hyperlipidaemia; infection; cancer; ful hyperactive disease; rheumatoid arthritis; osteoarthritis; systemic lupus erythematosuu; sepsis; asthma; allergic rhinitis; ischaemic heart disease; subarachnoid haemorrhage; viral hepatitis; AIDS.
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                                                                                                                                                                                                                                                                                                                                           activator of transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New signal transducer and activator of transcription 6 activation promoting purified protein, for diagnosing and treating disease associated with activation/inhibition of transcription factor e.g.
                                                                                                                                                                                                                                                                           Human cDNA encoding protein that promotes STAT6 activation #55
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human cDNA encoding a protein which promotes STAT6 activation.
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                                                                                                                                                                                                                                                                                                                                           gene; human; signal transducer and
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2002US-0385912P.
2002JP-00377326.
2002US-0436467P.
2003JP-00137505.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diabetes and cancer.
                                                                  ADI26144 standard;
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15-MAY-2003;
16-MAY-2003;
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1059 1119 1179 1239 1384 1299 1419 1479 1144 1264 1324 1359 1504 1564 1084 1204 965 ACACAGAGGCGTATAATCCCAAAATAAACGTGATGAACGCACCTTAATAAATCCAGATA 1024 579 939 666 459 519 664 724 639 784 669 844 759 819 879 604 904 964 ACATGATTCAGAAAACAAGAAACGCAAGTATTTCACCATAACCAGCTAGATTGGGATG 1565 AGACTGTGTCAGTCAACTAAACATTCTAATATTTTTGTAAACATTAAATTATTTTGTACA AAGCAGCTCGTTCAGAAATCCAAGTATTAGAGCACTTAAATAGTACTGATCCCAATAGTG TIGAACTATIGGGACTITAGIACTITACGACTICATIAAAGAAAATGGTTTTCTACCATTIC 845 GACTGGATCATATCAGAAAGATGGCATATCAGATATGCAAGTCTGTGAATTTTTTGCACA ATGTTTGGAGCATAGGTTGCATTCTTATTGAATATTACCTTGGTTTCACAGTCTTTCAGA CTCATGATAGTAAAGAGCACCTGGCAATGATGGAACGAATATTAGGACCCATACCACAAC ACATGATTCAGAAAACAAAACGCAAGTATTTTCACCATAACCAGCTAGATTGGGATG TTTGTCATGATGAACATGAGAACTGTTTGACCTGGTTCGAAGAATGTTAGAATATG AGACTGTGTCAGTCAACTAAACATTCTAATATTTTTGTAAACATTAAATTATTTTTGTACA ATGGCATGGATGCCATGCATGTAGCAGTGAAAATCGTAAAAATGTAGGCCGTTACCGTG <u>Araaagccccaccracacarcracacacraaaaracraaaaarcrccaracaracaracrcrc</u> AAGCTGCTCGCTCAGAATACAAGTTCTGGAACATCTGAATACAACAGACCCCAACAGTA TCTTCCGATGTGTCCAGATGCTAGAATGGTTTGATCATCATGGTCATGTTTGTATTGTGT crirccecrererccaearerrecaareerrreacarcarerreacarriccarrerr **TTGAACTACTGGGACTTAGTACTTACGAFTTTCATTAAAGAAAACAGCTTTCTGCCATTTC** AAATTGACCACATCAGGCGAGATGGGCGTATCAGATCTGCCAGTCAATAAATTTTTACATC ATAATAAATTTAACCCATACAGATCTGAAGCCTGAAAATATTTTGTTTTGTGAAGTCTGACT 905 GTAATAAGTTGACTCACACACACACTTAAAGCCTGAAAACATCTTATTTGTGCAGTCTGACT ATGTAGTCAAATATAATTCTAAAATGAAACGTGATGAACGCACACACTGAAAAACACAGATA TCAAAGTTGTTGACTTTGGAAGTGCAACGTATGATGATGAACATCACAGTACTTTGGTGT 1025 Tradastrictasactricstastastastaricareascarcacastastari CTACCCGGCACTACAGAGCTCCCGAGGTCATTTTGGCTTTAGGTTGGTCTCAGCCTTGTG CTCATGATAGTAAAGAGCACCTGGCAATGATGGAACGAATATTAGGACCCATACCACAAC AACACAGTTCTGCTGGTAGATATGTTAGGAGACGCTGCAAACCGTTGAAGGAATTTATGC AACACAGTTCTGCTGGTAGATATGTTAGGAGGCTGCTAGAACCGTTGAAGGAATTTATGC TTTGTCATGAAGAACATGAGAAACTGTTTGACCTGGTTCGAAGAATGTTAGAATATG AAAAGAAATGAAATGGGAATCAGTGGTCTTACTATACTTTCTTCTCTAGAAGAGATTACTTA AAAAGAAATGAAATGGGAATCAGTGGTCTTACTATATACTTCTCTAGAAGAGATTACTTA ATGAAATCGTGGACACTTTGGGTGAAGGAGCCTTTGGCAAAGTTGTAGAGTGCATTGATC Matches 1191; Conservative 1120 1505 580 1085 1000 1145 1060 1205 1265 1180 1325 1240 1385 1300 1360 1420 160 220 725 640 785 200 820 880 940 셤 8 g à ద à 셤 ò d ò ద ጵ 셤 ò Б ò 셤 ઠે 쉽 ð g ò 셤 ò g ò 셤 ö 셤 ò g ò 셤 ठे 셤 ઠે

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Length 1865;

Score 1118.8; DB 12; Pred. No. 8.3e-211;

47.5%;

Query Match Best Local Similarity

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The invention relates to a method of identifying compounds that influence fat cell number or size comprising providing a cell that expresses a gene and an agent, exposing the cell to the agent and identifying fat cell number or size relative to cells not exposed to the agent. The method also comprises providing an expression vector and an agent, exposing the vector to the agent, detecting a change in expression of the gene call attive to expression of the gene in an expression vector not exposed to the agent, treating a subject with the agent and identifying fat cell number or size in the subject comprises an antisense coligonucleotide. The subject comprises a mammal, preferably a human. The method also comprises providing a polypeptide and an agent, exposing the colypeptide to the agent, detecting binding of the agent to the subject that agent and identifying fat cell number or size in the subject unth the agent and identifying fat cell number or size in the subject. The agent comprises an antibody. A method of regulating fat cell number or size comprises providing a subject containing fat cells and an agent that changes the expression of a gene, and treating the subject with the agent under conditions so that fat cell size or number in the
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                                                                                                                                                                                                  CATGGAGGTCACCTCTGAAGTGATTTTTTTTGAGTAAAAGGAAATCTTGACTACTTTATA 1719
                                                                                                                                                                                                                    Identifying compounds that influence fat cell number or size for treating or preventing obesity or diabetes by exposing the cell to the agent and identifying fat cell number or size relative to cells not exposed to the
                   GTTAAGTGTAAATATTGTATGTATTGTATCAATAGCATAATTAACTTGTTAAGCAAGTAT
GTTAAGTGTAAATATTGTATGTTTTGTATCAATAGCATAATTAACTTGTTAAGCAAGTAT
                                                                                     GGTCTTGATAATGCATTAGAAAAATTAAAATTTAATTTTTCTTTTTGAAATTACCATTTTT
                                                                                                                                                     Mouse; gene, ss; fat cell number; fat cell size; obesity; diabetes; anorectic; antidiabetic.
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                                                                                                                                                                                                                                                                                                                      AD007812 standard; cDNA; 1446
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P-PSDB; ADO08029.
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subject is altered. The method is useful for identifying compounds that influence fat cell number or size, for preparing a composition for treating or preventing bosesity or diabetes. This sequence represents mouse cDNA used in the scope of the invention.
                                                                                                                                                                                                                                                                                                                                                                            AAAGATCCAGGAGTATAGAGGATGATGAGGAGGCTCACCTGATCTGTCAAAGTGGAGGCG
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                                                                Sequence 1446 BP; 461 A; 272 C; 352 G; 361 T; 0 U; 0 Other;
                                                                                       Score 1097.2; DB 12; Lengt
Pred. No. 1.4e-206;
0; Mismatches 118; Indels
                                                                                         Query Match
Best Local Similarity 90.8%;
Matches 1168; Conservative
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New human kinase proteins and nucleic acids, useful in drug screening assays, identifying modulators of kinase activity or treating disorders characterized by absence or unwanted expression of the protein.
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                     TCACAGTCTTTCAGACTCATGATAGTAAAGAGCACCTGGCAATGATGAAGAATATTAG 1104
                                                            GACCCATACCACACACATGATTCAGAAAACAAGAAAACGCAAGTATTTTCACCATAACC 1164
                                                                                                                                                                                                                                                                                                                                                                                             Human; kinase protein; enzyme; cytostatic; osteopathic; gene expression; colon-moderately differentiated adenocarcianoma; chromosome mapping; gene; drug screening; therapeutic; gene therapy; tissue typing; chromosome 5; bone osteosarcoma; single nucleotide polymorphism; SNP; ds.
                                1121 TCACAGTCTTTCAGACCCACGATAGTAAAGAGCACCCTGGCAATGATGAGGGGGGGATCTTAG
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standard_name= "Single nucleotide polymorphism"
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therapeutic agents that modulate kinase activity in cells and tissues
that express the kinase. The nucleic acids are useful as probes or
that express the kinase. The nucleic acids are useful as probes or
primers, in constructing recombinant vectors, for expressing antigenic
portions of the proteins, chromosome mapping, drug screening, testing an
individual for a genotype, and for gene therapy in patients containing
cells that are aberrant in kinase gene expression. The proteins may be
used in drug screening assays, in the identification of compounds that
modulate, stimulate or inhibit kinase activity, in pharmacogenomic
analysis, in treating disorders characterised by an absence or unwanted
corpusation of the protein (bone osteosarcoma, or colon-moderately
differentiated adenocarcinoma), and in generating antibodies specific for
the peptides. Such antibodies can be used to detect the protein in situ,
in vitro, or in cell lysate or supernatant, to isolate and purify the
proteins from host cells, pharmacogenomic analysis, tissue typing, and in
inhibiting protein function. The present sequence is human kinase protein
of therapeutic proteins and serve as targets for the development of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 21234 BP; 6065 A; 3772 C; 4258 G; 7139 T; 0 U; 0 Other;
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18917	2067	18977	2127	19037	2187	19097	2247	19157	2307	19217		
	TCTAACTGGAAAGTCAGCTTGGAAAATGGACATTTCCAAGTATGTTTGGTGAGTCACAGA	TCTAACTGGAAAGTCAGCTTGGAAAATGGACATTTCCAAGTATGTTTGGTGAGTCACAGA	TATAAAAATAGAAATTCTGATGAGAGGTTTCAGTTTTTAATACCAAGTCCTTAGGAGTCT	TATAAAAATAGAAATTCTGATGAGAGGTTTCAGTTTTTAATACCAAGTCCTTAGGAGTCT	TAACATTGGCCAGCATCTGTTTATCAAATGACATAAATACGTAAACCTATAAGAATTAAG	TAACATTGGCCAGCATCTGTTTATCAAATGACATAAATACGTAAACCTATAAGAATTAAG	TITATTAATTAGGGAATTTATGTCTGTGATAATTCTTACGGGAGAAAAGAGGGTTTGATTG	TITATTATTAGCAATTTATGTCTGTGATAATTCTTACGGGAGAAAGAGGTTTTGATTG	GAAAGCAGTTTGGGAAGAAGTGCTGCTGAAATTTCCAGAATTTAATTGGTTACAT	GAAAGCAGTTTGGGAAAGAAGTGCTGGTGAAATTTCCAGAATTTAATTGATTG	AAACTTTTTGACTTCAG 2324	AAACTITITIGACTITICAG 19234
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Search completed: March 16, 2005, 09:01:13 Job time : 1257.4 secs

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                                                                                                                                                                                                                                                                                     Description
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                           - nucleic search, using sw model
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Maximum DB seq length: 200000000
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases I to 1556)
Strausberg, R.L., Peingold, B.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, P.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
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Homo sapiens CDC-like kinase 4, mRNA (cDNA clone IMAGE:3908500),
containing frame-shift errors.
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/translation="MRHSKRTHCPDWDSRESWGHESYRGSHKRKRRSHSSTQENRHCK
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Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramon, R.D., Mullahy, S.J., Bosak, S.A., McBarah, P.J., McKernan, K.J., Male, J.A., Gunarante, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Schmutz, J., Myers, R.M., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIANL at: http://image.llnl.gov Series: IRAK Plate: 15 Row: d Column: 16
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 10190705
This clone has the following problem: frame shifted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         info@bcgsc.bc.ca

Eveven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,

Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,

Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo

Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven

Bess, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline

Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,

Michael Thorne, Miranada Isai, Natasja van den Bosch, Jill Vardy,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (15-OCT-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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/clone_lib="NIH_MGC_71"
/lab_host="DH10B"
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/db_xref="taxon:9606"
/clone="IMAGE:3908500"
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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Direct Submission
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1469 GAATGTTAGAATATGATCCAACTCAAGAATTACCTTGGATGAAGCATTGCAGCA 1345 TCTTTGACTTATTAAAAAGAAATGAAA 1372	LOCUS AY408252 1446 bp DNA linear GSS 15-DEC-2003 DEFINITION Home sapiens CLK4 gene, VIRTUAL TRANSCRIPT, partial sequence, GENOMIC SULVEY SEQUENCE. ACCESSION AY408252.1 GI:39764223 KEYWORDS GSS. SOURCE Home sapiens (human)	Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  AUTHORS clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,  Fortiera, S., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,  Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,  Adama, M.D. and Cargill, M.  TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios JOSIGES, 1960-1963 (2003)	AL SEED	Location/Qualifiers 1. 1446	vative ( TAGAAGCAAG TAGAAGCAAG GGAATGACTA GGAATGACTA ATCGAATCCA ATCGAATCCA ATCGAATCCA ATCGAATCCA ATCGAATCCA ATCGAATCCA GCAATAGACA	325 AAAGATCCAGGGGTATAGAGGATGATGAGGGCGTCACCTGATCTGTCAAAGTGGAGACG 384

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AK013974 1629 bp mRNA linear HTC 03-APR-200
Mus musculus 13 days embryo head cDNA, RIKEN full-length enriched
library, clone:3110002D09 product:CDC like kinase 4, full insert
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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SSAGRYVRRRCKPLKEFMLCHDEBHEKLFDLVRRMLEYDPTQRITLDEALQHPFPDLL

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                                                                        Euteleostomi;
                                                                                                                                                                          Z (bases I to 1865)
Zhao,M., Song,H., Li,N., Peng,Y., Han,Z. and Chen,Z.
Direct Submission
Submitted (18-15C-1999) Chinese National Human Genome Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai, 201203, People's Republic of China
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAGCAGCTCGTTCAGAAATCCAAGTATTAGAGCACTTAAATAGTACTGATCCCAATAGTG
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                                                                  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butele
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
1 (bases 1 to 1865)
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                                                                                                                        Zhao, M., Song, H., Li, N., Peng, Y., Han, Z. and Chen, Z. A novel gene expressed in human bone marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1118.8; DB 3; Length
Pred. No. 2e-220;
0; Mismatches 129; Indels
                                                                                                                                                                                                                                                                                                       1. .1865
/organism="Homo sapiens"
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/db_xref="taxon:9606"
/tissue_type="bone marrow"
154. .1515
                                                                                                                                                                                                                                                                                                                                                                                                                 codon start=1
GI:9437514
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                                     sapiens (human)
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Best Local Similarity 90.2
Matches 1191; Conservative
                                                       sapiens
                                                                                                                                                               Unpublished
                                       Homo
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TITLE JOURNAL

MEDLINE PUBMED REFERENCE AUTHORS MEDLINE PUBMED REFERENCE AUTHORS

JOURNAL

TITLE

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MLEWFDHHGHVCIVFELLGLSTYDPIKENSFLPFQIDHIRGMAYQICQSINFLHHNKL
THTDLKPENILIFVKSDYVKKNSKWKRDERTLKNTDIKVVDFGSATVDDEHHSTLVST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         translation="MDGLHVAVKIVKNVGRYREAARSEIQVLEHLNSTDPNSVFRCVQ"
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                                                                                                                                                                                                                                                                                                                                  /note="unnamed protein product; CDC like kinase 4 (MGD|MGI:1098551, GB|NM_007714, evidence: BLASTN, 99%,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GACGAATACAGGAATGACTACTGTGAAGGATATGTTCCTAGACATTATCACAGAGACATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1078.2; DB 3; Length 1629;
Pred. No. 4.9e-212;
0; Mismatches 183; Indels 103; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1629;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   264 AAGAGAAAGGGTAATAGACCCTGTGCAAGTCATCAGTCGCATTCG
                                                                                                                           /db_xref="FANTOM_DB:3110002D09"
/db_xref="taxon:10090"
/clone="3110002D09"
                                          musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /proteIn_id="BAC25420.1"
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'strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon start=1
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Best Local Similarity 82.5%;
Matches 1351; Conservative (
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Please visit our web site (http://genome.gsc.riken.jp/) for further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation 6 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The FANTOM Consortium and the RIKEN Genome Exploration Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             he RIKEN Genome Exploration Research Group Phase II Team and
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Meth. Enzymol. 303, 19-44 (1999)
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 1421)
Clark, A.G.; Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Fodd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wanog, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, White, T.J., Sninsky, J.J., Inferring nonneutral evolution from human-chimp-mouse orthologous
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Location/Qualifiers
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Mus musculus CLK4 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence. AY408254 AX408254.1 GI:39764225
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E 2 (Dases I to 1446)
S Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanembaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
Location/Qualifiers
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Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
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Pred. No. 5.3e-183;
0; Mismatches 346;
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/organism="Pan troglodytes"
                                                                     Science 302 (5652), 1960-1963 (2003)
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/db_xref="taxon:9598"
<1...1446
/gene="CLK4"
/locus_tag="HCM3162"
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Best Local Similarity 73.1%;
Matches 940; Conservative
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
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                                             625 ATGTTTGTATTGTGTTTGAACTACTGGGACTTAGTACTTACGATTTCATTAAAGAAAACA
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                        CTGATCCCAATAGTGTCTTCCGATGTGTCCAGATGCTAGAATGGTTTGATCATCATGGTC
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 Library
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Libra was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

Location/Qualifiers
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34.6%; Score 814.8; DB 3; Length
Best Local Similarity 73.4%; Pred. No. 1.2e-157;
Matches 1102; Conservative 0; Mismatches 382; Indels
                                                               1. 1737

Organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="crOBAOO9ZE09"

/tissue_type="placenta"

/plasmid="pcMVSPORT_6"
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Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage:
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
18t strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned
                                                                                                                                                                CR591789 1737 bp mRNA linear HTC 21-JUL-2004 full-length cDNA clone CL0BA009ZE09 of Placenta of Homo sapiens
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
Li, W. B., Gruber, C., Jessee, J. and Polayes, D.
Pull-length cDNA libraries and normalization
                                                                                 TTGTGAAGTCTGACTATGTAGTCAAATATAATTCTAAAATGAAACGGATGAACGCACAC
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http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
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1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
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Pred. No. 1.2e-157;
0; Mismatches 382;
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/organism="Homo sapiens"

/mol_type="taxon:9606"

/db_xref="taxon:9606"

/clone="CSODF036YH24"

/tissue_type="Fetal brain"

/plasmid="pCMVSFORT_6"
www.genoscope.cns.fr)
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Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage ;
BP 191 91006 EVRY cedex - FRANCE (E-mail ; segref@genoscope.cns.fr
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Li W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
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TITLE Direct Submission  JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :  BP 131 91006 EARY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)  COMMENT 1st strand cDNA was primed with a Not1-oligo(dT) primer. Five prime end enriched, double-serrand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.  FRATURES 11754   /organism="MRNA"   /organism="MRNA"   //organism="MRNA"   //organism="MRNA"   // // // // // // // // // // // // /	Query Match Best Local Similarity 73.4%; Score 814.8; DB 3; Length 1754; Best Local Similarity 73.4%; Pred: No. 1.2e-157; Matches 1102; Conservative 0; Mismatches 382; Indels 18; Gaps 4; Qy 84 AGTCATTATTAGAAGCTCCTTGAATGAGGAGATTATCGGGACCGGAGATACGT 143 Dh 238 AGCCATTATTTAGAAGCTAGAGTATATATAGAAAGATTAACGAAGATACACATACAATACAAAAGATAAAAAAAA	144 GACGAATACAGGAATGACTACTGTGAAGGATATGTTCCTAGACATTATCACAGAGACATT 2	DB 358 GAAAGCCGGTATCAGAACCATAGTAGCAAGTCTTCTGGTAGAAGTGGAAGTATAT 417  Qy 264 AAAAGGAAGCAATAGACACTGTTCAAGTCATCACGTTCGAAGAGCCAC 317  [	Qy         378 GGAGACGTTCTAAGAGCAAGATATGAAATCGTGGACACTTTGGGTGAAGGAGCCTTTGGC 437           Db         538 GGAGACGTACTAAGTGCAAGATATGAATTGTTGATACTTTAGGTGAAGGAGCTTTTGGA         597           Qy         438 AAAGTTGTAGAGTGCATTGATCATGCATGGATGCATGTAGCATGAAAAATGTA         497           Db         598 AAAGTTGTGGAGTGCATCGATCATAAAAGCGGGAGGTAGCATGTAGCAGTAAAAATAGTT         657	498   AAAAATGTAGGCCGTTACCGTGAAGCCCTCGTCAGAAATCCAAGTATTAGAGCCCTTA	
	Oy         1158         CATAACCAGGTAGATTGGGATGAACACAGTTCTGCTGGTAGATATGTTAGGAGGCTGC         1217           Db         1317         CACGATCGATTAGACTGGAACAGTTCTGCCGGCAGATATCTTCAAGACGTTT         1376           Oy         1218         AAACCGTTGAAGAATTTATGCTTTGTCATGATGAACATGAGAAAACTTTGACCTG         1277           Db         1377         AAACCTTGAAGAATTTATGCTTTGTCATGATGAACATGAGAGATGATGATCTTCTTTTATAGCTT         1436	1278 GTTCGAAGAATGTTAGAATATGATCCAACTCAAAGAATTACCTTGGATGAAGCATTGCAG 1437 ATTCAGAAAATGTTGGAGTATGATCCAGCCAAAAGAATTACTCTCAGAGAAGGAAG	DB 1497 CATCCTTTCTTTGACCTTCTGAGAGAAAGIATATGGACTTGGACA 1547  QY 1398 CTTCTCTAGAGAGATTACTTAAGACTGTGTCAGTCAACTAAACATTCTAATTTTT 1455  DB 1548 GCTCTCTCGAAGAGA-TCTTACAGACTGTATCGATTTTTAAATTTTAAATTTTTATTT 1606  QY 1456 GTAAACATTAAATTTTGTACAGTTAAGTGTAAATTTTGTATGATTTTGTATCATAGC 1515  DB 1607 TGTACAGCTTTGTAAATTCTTAACATTTTTAAATTGCCATGTTTTGTATTTTGTATTTTTTTAAATTTTTTTAAATTTTTGTATTTTTT		10 72 CR617 TION full- CION CR617 N CR617 N CR617 DS HTC;	SOURCE Homo sapiens (human) ORGANISM Homo sapiens ORGANISM Homo sapiens EUKaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; EUKaryota, Metazoa; Chordata; Catarrhini; Hominidae; Homo.  I (basee 1 to 1754) AUTHORS II, W.B., Gruber, C., Jessee, J. and Polayes, D.  TITLE Full-length cDNA libraries and normalization JOURNAL Unpublished REMARK Contact: Feng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/ InvitroGen.Corporation 1600 Faraday Avenue 2 (bases 1 to 1754) AUTHORS Genoscope.

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CDNA Library Preparation: Invitrogen Corp

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM14086 row: m column: 21

High quality sequence stop: 587.
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Fissue Procurement: Dr. David Rowe

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                                                                                                                                                                                                                                                                                         TTAGGTTGGTCTCAGCCTTGTGATGTTTGGAGCATAGGTTGCATTCTTATTGAATATTAC 1037
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  ATCTTATTTGTGCAGTCTGACTACACAGGGGGTATAATCCCAAAATAAAACGTGATGAA 1017
                                                                                                                                                                            GAACATCACAGTACTTTGGTGTCTACCCGGCACTACAGAGCTCCCGGAGGTCATTTTGGCT 977
                                                              CGCACACTGAAAACACACAGATATCAAAGTTGTTGACTTTGGAAGTGCAACGTATGATGATGT 917
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 973)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1398 CTTCTCTAGAAGAGATTACTTAAGACTGTGAGTC--AACTAAACATTCTAATATTTTT
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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AGENCOURT 10105484 NIH_MGC 134 Mus musculus cDNA clone
IMAGE:6513308 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (house mouse)
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BU516568
LOCUS
DEFINITION
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AUTHORS
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

6 (bases 1 to 1689)

8 Adachi,J., Aizawa,K., Akimura,T., Harah., Hashizume,W.,
Rukuda,S., Furuno,M., Hanagaki,T., Harah., Hashizume,W.,
Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
Koya,S., Kurihara,C., Matsuyama,T., Myazaki,A., Murata,M.,
Nakamra,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sakazume,N.,
Takeda,Y., Tanaka,T., Tawan,A., Takahashi,F., Takaku-Akahira,S.,
Tanaka,T., Tanaru,A., Towaru,A., Toya,T., Yasunishi,A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tissue type="placenta and extra embryonic tissue" /clone_lib="RIKEN full-length enriched mouse cDNA library" /dev_stage="18 days pregnant adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 143 TGACGAATACAGGAATGACTACTGTGAAGGATATGTTCCTAGACATTATCACAGAGACAT 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA library was prepared and sequenced in Mouse Genome broyclopedia Project of Genome Exploration Research Group in Rike Genomic Science Center and Genome Exploration of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            105. 1556
//note="PROTEIN KINASE CLK1 (EC 2.7.1.-) (CLK) (PROTEIN KINASE VARIASPENOT | P22518, evidence: PASTY, 95%ID, 100%length, match=1449)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    323 TGATGAATACAGGAATGACTACATG---GGCTACGAGCCAGGGCATCCCTATGGAGAACC
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Pred. No. 5.5e-141;
0; Mismatches 324; Indels
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URL:http://ganome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/etrain="C57BL/6J"
/db_xref="FANTOM_DB:3830430K12"
/db_xref="taxon:10090"
/clone="3830430K12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .1689
/organism="Mus musculus"
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/note="putative"
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Best Local S:
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Mus musculus 18 days pregnant adult female placenta and extra embryonic tissue cDNA, RIKEN full-length enriched library. Cilone:3830430K12 product:PROTEIN KINASE CLKI (EC 2.7.1.-) (CLK) (PROTEIN KINASE STY) homolog [Mus musculus], full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Komo, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
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                                                                                                                                                                                                                                                                                                                     1318 -CCTTGGATGAAGCATTGCAGCATCCTTTCTTTGACTTATTAAAAAAGAAATGAAATGGG 1376
                                                                                                                                                                                                                                                                                                                                                                                                                                    AATCAGTGGTCTTACTATATACTTCTCT-AGAAGAGATTACTTAAGACTGTGTGAGTCAA 1435
                                                                                          1198 GATATGTTAGGAGGCTGCAAACCGTTGAAGGAATTTATGCTTTGTCATGATGAAGAAC 1257
                                                                                                                                                                                                      1258 ATGAGAAACTGTTTGACCTGGTTCGAAGAATGTTAGAATATGATCCAACTCAAAGAATTA 1317
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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     845 TCTTTGGATGAAGCATTGCAGCACCCTTTCCTTGACTTTATAAAAAGAATTGAATGGGG
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                                                                                                                                                                                                                                                              786 ATGAGAAGCTGTTTGACCTGGTTC-AAAAATGTTGGAGTATGACCCACCGAGAAGGATCA
                                                                                                                                The RIKEN Genome Exploration Research Group Phase II Team and
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Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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HTC; CAP trapper.
Mus musculus (house mouse)
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/cell type="Lymphoblast-like"
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/lab host="Yoplof"
/clome lib="SIOSUU1"
/clome lib="SIOSUU1"
/clome lib="SIOSUU1"
/note="Organ: Stomach; Vector: pME18-FL3; Site_1: XhoI;
/clome lib="SIOSUU1"
/note="Organ: Stomach; Vector: pME18-FL3; Site_1: XhoI;
/note="Organ: Stomach; Vector: pME3 and then decapped with tabacco acid pyrophosphatase (TaP) . The decapped with Site by treatment of T4 RNA ligase and the first strand cDNA was synthesized with Superscript II using Sfil oligo-dT primer. After first strand synthesis, RNA was degraded by NaOH treatment and CDNA was amplified by PCR reaction. The PCR products were digested with Sfil and cloned into DraIII- digested pME185-FI3 vector. The obtained cDNA vectors were used for transformation of competent cells E. coli Toplof' by electroporation method. The CDNA libraries constructed by this method are full-length enriched CDNA library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and S.Im, Y.S.

21C Frontier Korean EST Project 2001
Unpublished (2002)
Contact: Kim YS
Genome Research Center
Korea Research Center
Korea Research Institute of Bioscience & Biotechnology
Fare Research Institute of Bioscience Project
Formation Yusecong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4410
                                                                        BM786882 722 bp mRNA linear EST 05-MAR-2002
K-EST0065716 S10SNU1 Homo sapiens cDNA clone S10SNU1-17-D07 5',
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Plate: 17 row: D column: 07
High quality sequence stop: 722.
Location/Qualifiers
e 1. 722
/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="S10SNU1-17-D07"
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    CCGAAGGAAAAGATCCAGGAGTATAGAGGATGATGAGGAGGGGCTCACCTGATCTGTCAAAG
                                                                            cccaaggaarraagccaagccracagacarcarcarcagaggaggaggarcarcarcagag
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TCAGCCTTGTGATGTTTGGAGCATAGGTTGCATTCTTATTGAATATTACCTTGGTTTCAC 1048
                                                                                                                            /tissue_type="airway or parenchyma"
/dev_stage="adult"
/clone lib="Rat lung airway and parenchyma cDNA libraries"
/note="Organ: lung; Vector: pGEM-11Zf(-); Site_1: Eco RI;
Site_2: Not I; mRNA was isolated from microdissected rat
lung airways and parenchyma tissues."
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              /organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db xref="taxon:10116"
/clone="Contig3421"
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Rattus norvegicus cDNA clone Contig3421 5', mRNA sequence.
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Average Phred score is 20 or better. All poor quality data (Phred
20) and vector/linker sequence has been removed.
High quality sequence stop: 966.
Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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L. Am. J. Respir. Cell Mol. Biol. 30 (3), 296-310 (2004)
Contact: Shultz MA
Dept. of Molecular Biosciences, School of Veterinary Medicine University of California, Davis
1311 Haring Hall, One Shields Avenue, Davis, CA 95616, USA Fax: 530 752 0793
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                                  241 ATCACAGTACTTTGGTGTCTACCGGCACTACAGAGCTCCCGAGGTCATTTTGGCTTTTAG
                                                                                                                                                                      GITGGICTCAGCCTTGTGATGTTTGGAGCATAGGTTGCATTCTTATTGAATATTACCTTG
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Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 2117 Std Error: 0.00
Seq primer: -40ml3 fwd. BT from Amersham

High quality sequence stop: 475.
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/lab host="hilloB"
/lab host="hilloB"
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/clone lib="NCI_CGAP_Br2"
/note="Vector: pTTT3D-Pac (Pharmacia) with a modified
polylinker; lst strand cDNA was prepared from pooled bulk
breast tumor tissue, and was then primed with a Not I -
oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pTTT3
vector. This library is the normalized version of
NCI_CGAP_Br1.1. Library was constructed by Bento Soares
and M. Fātima Bonaldo. "
                                                                                                                                                                                                                                                                                       AA631990 727 bp mRNA linear EST 28-OCT-1997 np74a05.sl NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1132016 3' similar to SW:KCLK_MOUSE P22518 PROTEIN KINASE CLK ;, mRNA
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                                                CTCAGCCTTGTGATGTTTGGAGCATAGGTTGCATTTTTTGAATATTACCTTGGTTTCA 1047
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                                                                                         840 ATTGCCATTTTTAAAGGCCTTTACAGTGCCCTTTGTGTCCAGTGGTAAACGTGATTGGTC 899
    180 TIAAGTATGGTGTTGATAATGAATGCAATATGAGTTAAAATGGATTTTCCTTTGATGTTA 839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Euthoria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 727) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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AA631990.1 GI:2555404
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Unpublished (1997)
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4385, Ap 9631, Ap 2299, Ap 3590, Ap 15332, Ap 1168, Ap 518, App 11373, A

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22, Appl 13504, A 12378, A

13, Appl 17296, A

14390, A 14391, A

15940, A

Sequence Seq

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; Sequence 1, Application US/09810671
; Patent No. 6455291
; GREERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCEBIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; TITLE OF INVENTION: THEREOF
; TITLE OF INVENTION: ACID 001566
; CURRENT APPLICATION NUMBER: US/09/810,671
; CURRENT PILLING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO
; SEQ ID NO
; LENGTH: 2354
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100.0%; Pred. No. 0;
tive 0; Mismatches
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; ORGANISM: Human
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Sequence 24, Appl
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US-09-029-22

US-09-905-999-22

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100.0%; Score 2354;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2354; Conservative 0; Mismatches
CURRENT FILING DATE: 2002-04-01
PRIOR APPLICATION NUMBER: 60/227,470
PRIOR FILING DATE: 2000-08-24
PRIOR PELLING DATE: 2001-03-19
PRIOR FILING DATE: 2001-03-19
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.
                                                                                                ; TYPE: DNA
; ORGANISM: Homo sapien
US-10-109-854-1
                                                                                      LENGTH: 2354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NATA:
APPLICATION NATA:
APPLICATION NATA:
APPLICATION NUMBER: US/09/016,000
FILING DATE: HEREWITH
CLASSIFICATION NUMBER:
FILING DATE:
ATTOMNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                               APPLICANT: Lal, Preeti
APPLICANT: Bandman, Olga
APPLICANT: Akerblom, Ingrid E.
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl G.
TITLE OF INVENTION: PROTEIN KINASE MO
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                 SSEE: Incyte Pharmaceuticals,
1: 3174 Porter Drive
Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: PF-0465
TELECOMMUNICATION INFORMATION:
                                                                                                       US-09-016-000-9
; Sequence 9, Application US/09016000
; Patent No. 5962232
                                                                                                                                                                                           Hillman, Jennifer L
Lal, Preeti
Bandman, Olga
Akerblom, Ingrid E.
Shah, Purvi
2341 AACAAAAAAAAAC 2354
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TELEFAX: 650-845-4166
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LENGTH: 2446 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 95.8
Matches 2155; Conservative
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear IMMEDIATE SOURCE: LIBRARY: NEUTFMT01 CLONE: 339963
                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Hillmar
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STREET: 31
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Sequence 26, Application US/09905999

Patent No. 6797513

GENERAL INFORMATION:
APPLICANT: ULLRICH, Axel
APPLICANT: NAYLER, Oliver
TITILE OF INVERTION: CLK PROTEIN KINASES AND RELATED PRODUCTS AND METHODS
FILE REFERENCE: 038602/0431

CURRENT APPLICATION NUMBER: US/09/905,999
CURRENT FILING DATE: 1001-07-17

PRIOR APPLICATION NUMBER: PCT/1B97/00946

PRIOR FILING DATE: 1997-06-17

PRIOR FILING DATE: 1997-06-17

PRIOR FILING DATE: 1997-06-17

PRIOR FILING DATE: 1997-06-17

PRIOR APPLICATION NUMBER: US 08/877,150

PRIOR FILING DATE: 1997-06-17

PRIOR APPLICATION NUMBER: US 60/034,286
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APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
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Pred. No. 4.7e-286;
0; Mismatches 3; Indels 1;
                                                                                                                                                                                                                                                                                  ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
CLASSIFICATION:
                                                                                                                                                                                    ADDRESSEE: INCYTE PHARMACEUTICALS, INC. STREET: 31.4 PORTER DRIVE CITY: PALO ALTO STATE: CALIFORNIA COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION UMBER: 37,01
REFERENCE/DOCKET NUMBER: PA-001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (50) 855-0555
INFORMATION FOR SEQ ID NO: 699:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
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| IMMEDIATE SOURCE:
| LIBRARY: HNT2AGT01
| CLONE: 488842
| US-09-023-655-699
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Best Local Similarity
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Patent No. 6455291
GENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, FITILE OF INVENTION: THEREOF
FILE REFERENCE: CLO00758
CURRENT APPLICATION NUMBER: US/09/810,671
CURRENT FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FASTESEQ for Windows Version 4.0
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Best Local Similarity 100.0%; Pred. No. 4.4e-265;
Matches 1097; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                      TCTTTGACTTATTAAAAAGAAATGAAATGG 1375
                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
CRGANISM: Human
US-09-810-671-3
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LENGTH: 21234
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46.6%; Score 1097.4; DB 4; Length 1549;
Best Local Similarity 90.6%; Pred. No. 9.9e-266;
Matches 1170; Conservative 0; Mismatches 121; Indels 0:
PRIOR FILING DATE: 1996-12-19
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin version 3.0
SEQ ID NO 26
LENGTH: 1549
                                                                       TYPE: DNA
CORGANISM: Mus musculus
US-09-905-999-26
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                                                                                                                                                           46.6%; Score 1097; DB 4; L 100.0%; Pred. No. 4.4e-265; Live 0; Mismatches 0;
                      Version
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FRRESEQ for Windows
SEQ ID NO 3
LENGTH: 21234
                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 1097; Conservative
                                                                            TYPE: DNA
; ORGANISM: Homo sapien
US-10-109-854-3
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                                                                              ACTAGAAACCAAAAACTCAGAAAATGTTTACTGTTAGAATTCTATTAAATTTTAAGTGTTG
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                      GACTACTTTATATTCTTAAAGGAATATTCTTTATATACTTCAAATTTAGAACTTAACTTT
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Fatent No. 6727066
GENERAL INFORMATION:
APPLICANT: Kaser, Matthew R.
TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
FILE REFERENCE: PA-0035 US
CURRENT APPLICATION UNMBER: US/09/919,039
CURRENT APPLICATION NUMBER: 60/222,113
PRIOR APPLICATION NUMBER: 60/222,113
PRIOR APPLICATION NUMBER: 60/222,113
SOFTWARE: PERL PROGRAM
SEQ ID NOS: 401
SOFTWARE: PERL PROGRAM
TENDEM 10 238
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                                                                                     TATICITITICATIGGGIGATGICAGGGIGATAACCAGACATICATGGAAAGGCATGCAG
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OTHER INFORMATION: Incyte ID No. 6727066 420527.25
FEATURE:
NAME/KEY: unsure
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US-09-919-039-238
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GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES;

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES;

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES;

CURRENT APPLICATION NUMBER: US/10/339,656

CURRENT FILING DATE: 2003-01-10

PRIOR FILING DATE: 2001-03-19

PRIOR FILING DATE: 2001-03-19

PRIOR FILING DATE: 2001-03-19

PRIOR PLILING DATE: 2001-03-19

PRIOR PLILING DATE: 2000-08-24

NUMBER OF SEQ ID NOS: 5

SOFTWARE: PRECED FREEDOM WINDOR: 5

SECTIVARE: PRECED FREEDOM WINDOR WIN
                                                                                                                          .9098 TITATTAATTAGGCAATTTGTCTGTGATAATTCTTACGGGAAAGAGGATTTGATTG 19157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/10339656
Patent No. 6733978
                                                                                                                                                                                                                                                                                                                                                             2308 AAACTTTTGACTTCAG 2324
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ORGANISM: Homo sapien
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GENERAL INFUGRATION
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TITLE OF INVENTION: CLK PROTEIN KINASES AND RELATED PRODUCTS AND METHODS
TITLE OF INVENTION: CLK PROTEIN KINASES AND RELATED PRODUCTS AND METHODS
FILE REFERENCE: 038602/0431
CURRENT APPLICATION NUMBER: US/09/905,999
CURRENT FILING DATE: 1999-07-31
PRIOR APPLICATION NUMBER: PCT/IB97/00946
PRIOR APPLICATION NUMBER: PCT/IB97/0617
PRIOR APPLICATION NUMBER: US 08/877,150
PRIOR APPLICATION NUMBER: US 08/877,150
PRIOR FILING DATE: 1997-06-17
PRIOR FILING DATE: 1996-12-19
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PALENTIN VERSION 3.0
SEQ ID NO 22
TENNETH. 1538
                                                                                                                                                 2052
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TAACATTTTTATTTGCCATGTTTATTTTGGTAATTTGGTTCATTAAGTACATAG 2112
                                                                                        TAAGACTGTGTCAGTC--AACTAAACATTCTAATATTTTTGTAAACATTAAATTTTTG 1475
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Pred. No. 7.9e-111;
0; Mismatches 398;
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Patent No. 6797513
GENERAL INFORMATION:
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Best Local Similarity 64.6
Matches 736; Conservative
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; ORGANISM: Mus musculus
US-09-905-999-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 11
US-09-905-999-22
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Pred. No. 8e-151;
0; Mismatches 329; Indels
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                                       g, or other
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Best Local Similarity 72.1%;
Matches 880; Conservative
      ; LOCATION: 231, 241
; OTHER INFORMATION: a, t, c,
US-09-919-039-238
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PRIOR FILING DATE: 1996-12-19
NUMBER OF SEQ ID NOS: 26
SOFFWARE: Patentin version 3.0
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                                                                                                                                              Conservative
                                                               TYPE: DNA
CORGANISM: Mus musculus
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Sequence 24, Application US/09905999

Patent No. 6797513

GENERAL INFORMATION:

APPLICANT: ULLRICH, Axel

TITLE OF INVENTION: CLK PROTEIN KINASES AND RELATED PRODUCTS AND METHODS

FILE REFERENCE: 036602/0431

CURRENT APPLICATION NUMBER: US/09/905,999

CURRENT FILING DATE: 1001-07-17

PRIOR APPLICATION NUMBER: PCT/1B97/00946

PRIOR FILING DATE: 1997-06-17

PRIOR APPLICATION NUMBER: US/08/11/150

PRIOR APPLICATION NUMBER: US/08/17/150

PRIOR FILING DATE: 1997-06-17

PRIOR FILING DATE: 1997-06-17

PRIOR APPLICATION NUMBER: US/08/4,286
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                                       TTGTGTTTGAACTACTGGGACTTAGTACTTACGATTTCATTAAAGAAAACAGCTTTCTGC
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      Length
Score 454.8; DB 4; Length
Pred. No. 3.7e-104;
0; Mismatches 362; Indels
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Sequence 2648, Application US/09949016; Patent No. 6812339; Caneral Information:
, Applicant: VERMATION:
, TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
, TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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                                          560 CAAGGTGGTGGAGTGCTTGGACCATGCCAGAGGGAAGTCTCAGGTTGCCCTGAAGATCAT
                                                                                         197 AAAAAATGTAGGCCGTTACCGTGAAGCAGCTCGTTCAGAAATCCAAGTATTAGAGCACTT
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; Batent No. 6500938
; GENERAL INFORMATION:
    APPLICANT: Janice Au-Young
    APPLICANT: Jeffrey J. Seilhamer
    TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
    TITLE OF INVENTION: PATHWAY GENE EXPRESSION
    NUMBER OF SEQUENCES: 1490
    CORRESPONDENCE ADDRESS:
    ADDRESSE: INCYTE PHARMACEUTICALS, INC.
    STREET: 3174 POPTER DRIVE
    CITY: PALO ALTO
    STREET: ALLO ALTO
    STREET: ALLO ALTO
    STREET: ALLO FORTER DRIVE
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COMPUTER: IEM PC Compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
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NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REPERENCE/DOCKET NUMBER: PA-0002 US
TELECOMUNICATION INFORMATION:
TELECHONE: (650) 845-0555
INFORMATION FOR SEQ ID NO: 1439:
SEQUENCE CHARACTERISTICS:
LENGTH: 1762 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
                                                                                                                                                                                          1337 GCATCCTTTCTTTG 1350
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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STRANDEDNESS: single
TOPOLOGY: linear
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
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US-09-016-434-1439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
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                                                                                                                                                                                                                                                                                                             RESULT 13
US-09-016-434-1439
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Sequence 2649, Application US/09949016

patent No. 6812339

GENBRAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHIGMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

FILE REFERENCE: CLOO01307

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,756

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-09-08

NUMBER OF SEQ ID NOS: 207012

SOUTHWARE: FESTSEQ for Windows Version 4.0
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                                     1220 GATCCTAGGGCCCATCCCATCACAGATCCACGGACAGAAGAAATATTTCTA
                                                                                                                            1097 AATATTAGGACCCATACCACACACACATGATTCAGAAAACAAGAAAACGCAAGTATTTTCA
                                                                                                                                                                                       CAAACCGTTGAAGGAATTTATGCTTTGTCATGATGAAGAACATGAGAAACTGTTTGACCT
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Best Local Similarity 63.5
Matches 657; Conservative
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ORGANISM: Human
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US-09-949-016-2649
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LENGTH: 1763
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Pred. No. 3.9e-98;
0; Mismatches 377; Indels
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FREESEQ for Windows Version 4.0
SEQ ID NO 2648
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Best Local Similarity 63.5%;
Matches 657; Conservative 0
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US-09-949-016-2648
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Best Local ?
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                                    800 GGAGAATAACTTCCAGCCTTACCCCTACCACATGTCCGGCACATGGCCTACCAGCTCTG 859
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7 US-10-641-643-699
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GenCore version
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Maximum Match 100%
Listing first 45 summaries
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## ALIGNMENTS

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Sequence 1, Application US/09810671
Publication No. US20020076783A1
GENERAL INFORMATION:
CENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: THEREOF
FILE REPERRNCE: CLOOOTS
CURRENT APPLICATION NUMBER: US/09/810,671
CURRENT PILLIA DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FRASEC FOR WINDOWS Version 4.0
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Result No.

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| Publication No. US20020119548A1 |
| GENERAL INFORMATION |
| GENERAL INFORMATION |
| GENERAL INFORMATION |
| TITLE OF INVENTION | SCLATED HUMAN KINASE PROTEINS, NUCLEIC |
| TITLE OF INVENTION | ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES |
| TITLE OF INVENTION | THRREOF |
| TITLE OF INVENTION | THRREOF |
| TITLE OF INVENTION | THRREOF |
| CURRENT FILING DATE: 2002-04-01 |
| PRIOR APPLICATION NUMBER: 60/227,470 |
| PRIOR APPLICATION NUMBER: 09/910,671 |
| PRIOR FILING DATE: 2001-03-19 |
| NUMBER OF SEQ ID NOS: 5 |
| SEQ ID NO 1 |
| LENGTH: 2354
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    Score 2354;
Pred. No. 0;
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    100.0%;
Query Match
Best Local Similarity 100.
Matches 2354; Conservative
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	RESULT 4 US-10-801-671-1 Sequence 1, Application US/10801671 Sequence 1, Application US/10801671 Sequence 1, Application No. US20040152123A1 GENERAL INFORMATION: TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES TITLE OF INVENTION: THEREOF FILE REFERENCE: CLO00758DIV-III CURRENT FILING DATE: 2004-03-17 PRIOR FILING DATE: 2004-03-17 PRIOR PRILING DATE: 2000-08-24 PRIOR FILING DATE: 2001-03-19 NUMBER OF SEQ.ID NOS: 5 SOFTWARE: FeatSEQ for Windows Version 4.0 SEQ ID NO 1 LENGTH: 2354 TYPE: DNA CREANISM: Homo sapiens US-10-801-671-1	Query Match         100.0%;         Score 2354;         DB 18;         Length 2354;           Best Local Similarity 100.0%;         Pred. No.0;         <	Qy         61 CTGTTGAAGAGCACACTCATCCCAGTCATTTAGAAGCAAGGTCCTTGAATGAGGGGG         120           Db	QY         181 CTAGACATTATCACAGAGACATTGAAAGGGGGTATCGATTGCATTGCAGTCACTTGCAGTAAATCTTCAG         240           Db         181 CTAGACATTATCACAGAGACATTGAAAGCGGGTATCGAATCCACTGCAGTAAATCTTCAG         240           QY         241 TCCGCAGCAGGAGAAGCGAGTCGCAATAGACACTGTTCAAGTCATCAGT         300           Db         241 TCCGCAGCAGGAGAAGCGCAATAGACACTGTTCAAGTCATCAGT         300	OY 301 CACGTTCGAAGAGCCACCGAAGGAAAAGATCCAGGAGTATAGAGGAGGATGGTGAGGAGGGTC 360
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	TAGATHGETTIGATCATGTGTTGTTTGTTTTTTGAACTGGGGACTTGTTTGT	ATCTGAAGCCTGAAAATATTTGTTTGTGAAGTCTGACTATGTAGTGAAATATAAAAAAACACAGATATCAAAGTGTGAAATATAAAAAACACAGATATCAAAGTTGTTGACTTTGTTGTGAACTTGAAGAAAACACAGATATCAAAGTTGTTGACTTTGAAGAAACACAGAAAACACAGAAAACACAGAAAACACAAAAACACAAAAAA	CCGAGGTCATTTTGGCTTTAGGTTGGTCTTCAGACTTTGGAGGTTGGAGGTTGGATTGAGAAAAGAGAATTGGCAATGATTGAGAAAAGAAAAAAAA	141	1321 TGGATGAAGCATTGCAGCATCCTTTCATTAAAAAAGAAATGAAATGAGAATC 1380  1321 TGGATGAAGCATTGCAGCATCCTTTCTTTGACTTATTAAAAAAGAAATGAAATGGGAATC 1380  1381 AGTGGTCTTACTATACTTCTCTAGAAGAGATTACTTAAGACTGTGTCAGCCAACTAAA 1440

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                                                                                                                  ; OTHER INFORMATION: Clone ID: LIB4654-056-G4_FLI
US-10-425-114-26852
                                                                                                                                       Score 1908.4;
Pred. No. 0;
0; Mismatches
                                                                                                                                       81.1%;
99.9%;
                                                                                                                                       Query Match
Best Local Similarity 99.9
Matches 1909; Conservative
                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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         881 TTGTGAAGTCTGACTATGTAGTCAAATATAATTCTAAAATGAAACGTGATGAACGCACAC 940
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Publication No. US20040077003A1
GENERAL INFORMATION
APPLICANT: Cocks, Benjamin G.
Susan G. Stuart
Jeffrey J. Salhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC Compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
COPRAPTING SYSTEM: PC-DOS/MS-DOS 6.2
SOFTWARE: WORD PERFECT 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/641,643
FILING DATE: 14-ANG-2003
CLASSIFICATION: CURKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: INCYTE PHARMACEUTICALS,
STREET: 3174 PORTER DRIVE
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APPLICATION NUMBER: <Unknown>
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
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CORRESPONDENCE ADDRESS:
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STATE: CALIFORNIA
COUNTRY: USA
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100.0%; Pred. No. 1.7e-255;
ive 0; Mismatches 0; Indels 0;
                                       Sequence 135, Application US/10267502
Publication No. US20040071700A1
GENERAL INFORMATION:
APPLICANT: Kim, Jaeseob
APPLICANT: Kim, Jaeseob
TITLE OF INVENTION: Obesity Linked Genes
FILE REFRENCE: LSD-07416
CURRENT APPLICATION NUMBER: US/10/267,502
NUMBER OF SEQ ID NOS: 439
SOUTHARE: PatentIn version 3.2
SEQ ID NO 135
LENGTH: 1446
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Matches 1286; Conservative
                                                                                                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-267-502-135
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Sequence 26, Application US/09905999;
Sequence 26, Application US/09905999;
Sequence 26, Application US/09905999;
Patent No. US20020106771A1
GENERAL INFORMATION:
APPLICANT: ULLRICH, Axel
APPLICANT: NAYLER, Oliver
TITLE OF INVENTION: CLK PROTEIN KINASES AND RELATED PRODUCTS AND METHODS
FILE REPERENT 2001-07-17
CURRENT APPLICATION NUMBER: US/09/905, 999
CURRENT FILING DATE: 1999-07-31
PRIOR PILING DATE: 1999-07-31
PRIOR APPLICATION NUMBER: US 08/877,150
PRIOR APPLICATION NUMBER: US 08/877,150
PRIOR PILING DATE: 1997-06-17
PRIOR PRILING DATE: 1997-06-17
PRIOR PILING DATE: 1997-06-17
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PRIOR PILING DATE: 1997-06-17
SPRIOR PILING DATE: 1997-06-17
PRIOR PILING DATE: 1997-06-17
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Best Local Similarity 90.6
Matches 1170; Conservative
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CORGANISM: Mus musculus
US-09-905-999-26
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US-09-905-999-26
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Pred. No. 3.2e-233;
0; Mismatches 3; Indels
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUTICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEPAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 699:
SEQUENCE CHARACTERISTICS:
LENGTH: 1456 base pairs
TYPE: nucleic acid
STRANDENESS: single
TYPE: nucleic acid
STRANDENESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LENGTH: LIBRARY: HNIZAGT01
                                                                                                                                                                                                                                                                                                                      SEQUENCE DESCRIPTION: SEQ ID NO: 699
US-10-641-643-699
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Best Local Similarity 99.7%;
Matches 1191; Conservative
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APPLICANT: ULLRICH, Axel
TITLE OF INVENTION: CLK PROTEIN KINASES AND RELATED PRODUCTS AND METHODS
TITLE REPERENCE: 038602/0431
CURRENT FILING DATE: 2004-04-16
CURRENT FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: US/09/905,999
PRIOR PILING DATE: 1999-07-31
PRIOR PILING DATE: 1999-07-31
PRIOR PILING DATE: 1999-06-17
PRIOR PILING DATE: 1997-06-17
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PRIOR PILING DATE: 1999-106-17
PRIOR PILING DATE: 1999-106-17
PRIOR PILING DATE: 1996-12-19
NUMBER OF SEQ ID NOS: 26
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Pred. No. 1.7e-216;
0; Mismatches 121; Indels
 1499 TCTTTGACTTATTAAAAGGAAATGAGTGGG 1529
                                                                                         Sequence 26, Application US/10825177; Publication No. US20040259220A1; GENERAL INFORMATION:
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Best Local Similarity 90.6%;
Matches 1170; Conservative (
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CORGANISM: Mus musculus
US-10-825-177-26
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Publication No. US20040071700A1
GENERAL INFORMATION:
APPLICANT: Kim, Jaeseob
APPLICANT: Galant, Ron
TITLE OF INVENTION: Obesity Linked Genes
FILE REFREENCE: LSD-07416
CURRENT APPLICATION NUMBER: US/10/267,502
CURRENT FILING DATE: 2003-01-27
NUMBER OF SEQ ID NOS: 439
SEQ ID NO 138
LENGTH: 1446
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Mismatches 118; Indels
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19098 TITATITAATITAGGCAATITATGTCTGTGATAATICTTACGGGAGAAAGAGATITGATIG 19157
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TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION NUMBER: 08/10/109,854
CURRENT APPLICATION NUMBER: 60/227,470
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: 09/810,671
PRIOR FILING DATE: 2001-03-19
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FASSESQ for Windows Version 4.0
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                                                                               ACTAGAAACCAAAACTCAGAAAATGTTTACTGTTAGAATTCTATTAAATTTTAAGTGTTG
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100.0%; Pred. No. 6.7e-216;
iive 0; Mismatches 0;
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Matches 1097; Conservative 0; Mismatches
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; Sequence 3, Application US/10109854
; Publication No. US20020119548A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapien
US-10-109-854-3
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                                                                                                                                                   Sequence 3, Application US/09810671
; Sequence 3, Application WS/020076783A1
; GENERAL INFORMATION:
; APPLICANT: YAM, CHUMHUA et al
; TITLE OF INVENTION: ISCLID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES;
; TITLE OF INVENTION: THEREOF
; TITLE OF INVENTION: THEREOF
; FILE REPRENCE: CLORO758
; CURRENT APPLICATION NUMBER: US/09/810,671
; CURRENT PILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 21234
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                                                                  TGAAGGAATTTATGCTTTGTCATGATGAAGAACATGAGAAACTGTTTGACCTGGTTCGAA 1284
   AGCTAGATTGGGATGAACACAGTTCTGCTGGTAGATATGTTAGGAGACGCTGCAAACCGT
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46.6%; Score 1097; DB 9; Length 2
Best Local Similarity 100.0%; Pred. No. 6.7e-216;
Matches 1097; Conservative 0; Mismatches 0; Indels
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; ORGANISM: Human
US-09-810-671-3
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J. GENERAL INCLULIANT
J. CENTRALL INCLULIANT
J. CENTRALL INCLULIANT
J. TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
CURRENT APPLICATION NUMBER: US/10/339,656
CURRENT APPLICATION NUMBER: 10/109,854
PRIOR FILING DATE: 2003-01-10
PRIOR FILING DATE: 2001-03-19
PRIOR FILING DATE: 2001-03-19
PRIOR FILING DATE: 2001-03-19
PRIOR FILING DATE: 2000-08-24
NUMBER OF SEQ. ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ. ID NOS: 3
LENGIT 21234
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                                                                                          Sequence 3, Application US/10339656
Publication No. US20030134319A1
GENERAL INFORMATION:
TYPE: DNA
CORGANISM: Homo sapien
US-10-339-656-3
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US-10-425-114-26212
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; Sequence 3, Application US2004015212341
; Publication No. US2004015212341
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS,
; TITLE OF INVENTION: THEREOF
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CLO00758DIV-III
CURRENT FILING DATE: 2004-03-17
; PRIOR APPLICATION NUMBER: 09/810,671
; PRIOR PILING DATE: 2000-08-24
; PRIOR FILING DATE: 2001-03-19
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PRECED FOR Windows Version 4.0
; SEQ ID NO S: 5
; SOFTWARE: PRECED FOR WINDOWS SECOND AS A SECOND A
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ORGANISM: Homo sapiens
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                                                      APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Screen, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
CURRENT FILING DATE: 2003-04-28
SEQ ID NO 26:212
LENGTH: 3040
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 977.4; DB 17; Length 3040;
Pred. No. 1.4e-191;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Clone ID: LIB4115-001-H8_FLI
US-10-425-114-26212
Sequence 26212, Application US/10425114
Publication No. US20040034888A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 99.9%;
Matches 978; Conservative C
                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Homo sapiens
                                         GENERAL INFORMATION:
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1357 3021 1177 2901 2841 GCTTTGTCATGATGAAGAACATGAGAAACTGTTTGACCTGGTTCGAAGAATGTTAGAATA 1297 GCTTTGTCATGATGAAGAACATGAGAAACTGTTTGACCTGGTTCGAAGAATGTTAGAATA 2961 TGAACACAGTTCTGCTGGTAGATATGTTAGGAGGCGGCTGCAAACCGTTGAAGGAATTTAT 1237 ACACATGATTCAGAAAAACAAGAAAACGCAAGTATTTTCACCATAACCAGCTAGATTGGGA TGAACACAGTTCTGCTGGTAGATATGTTAGGAGGACGCTGCAAACCGTTGAAGGAATTTAT ACACATGATTCAGAAAACAAGAAAACGCAAGTATTTTCACCATAACCAGCTAGATTGGGA Search completed: March 17, 2005, 00:47:18 Job time : 1320.36 secs AAAAAAGAAATGAAATGGG 1376 3022 AAAAAAGAAATGAAATGGG 3040

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Copyright (c) 1993 - 2005 Compugen Ltd.
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1 MCIPLEASHSVEEDTHPSHY.....QRITLDEALQHPFFDLLKKK 445

Title: Perfect score: Sequence: Scoring table:

2105692 segs, 386760381 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

2105692 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A Geneseq 16Dec04:\*

1: geneseqp1980s:\*
2: geneseqp2000s:\*
4: geneseqp2001s:\*
5: geneseqp2001s:\*
6: geneseqp2003as:\*
7: geneseqp2003as:\*
8: geneseqp2003as:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	Aae20170 Human kin	Adi26143 Human pro	Ado08026 Human pol	Adp24394 PRO polyp	Hume	Adi26141 Human pro	Ado08029 Mouse pol	Aaw49914 Mouse CLK	Aab65648 Novel pro	Adi29255 Human MAR	Human	Human	Serin	Adh58849 Human CDC	-	Adp24719 PRO polyp	0	1 Mouse	Adi26145 Human pro	1 Mouse	Adg74657 Human kin	Aab33778 Human sec	Aab58831 Breast an	Aab33777 Human sec	Aae37967 Human kin
ID	AAE20170	AD126143	AD008026	ADP24394	AAB69705	ADI26141	ADO08029	AAW49914	AAB65648	ADI29255	AAY27054	ADO08027	AAU75108	ADH58849	ADR14001	ADP24719	ADO08030	AAW49911	ADI26145	AD008031	ADG74657	AAB33778	AAB58831	AAB33777	AAE37967
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& Query Match	100.0	96.1	96.1	96.1	95.2	93.8	93.5	90.4	88.3	88.3	87.9	78.5	78.3	78.3	78.3	78.3	75.6	75.0	74.8	66.7	64.3	63.7	63.3	62.9	59.0
Score		2315.5	2315.5	2315.5	2294.5		2252.5		2127.5	2127.5	2117.5	1893	1887	1887	1887	1887	1823	1808.5	1803	1607	1549	1535	1526	1517	1422.5
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## ALIGNMENTS

RESULT 1

E	AAE20170
	AAE20170 standard; protein; 445 AA.
{¥}	AAE20170;
<b>结</b>	18-JUN-2002 (first entry)
<b>2</b> 图 3	Human kinase protein.
<b>≨ ≩ §</b>	Human; kinase protein; enzyme; cytostatic; osteopathic; gene expression; colon-moderately differentiated adenocarcinoma; chromosome mapping; dene;
ž	drug screening; therapeutic; gene therapy; tissue typing; chromosome 5;
₹	bone osteosarcoma.

oma.				Location/Qualifiers	• • • • • • • • • • • • • • • • • • • •
Done osteosarcoma		OS Homo sapiens.			
pone		Ношо		Key	
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	Location/Qualifiers	10, .13	/note= "Casein kinase II phosphorylation site"	2431	/note= "Tyrosine kinase phosphorylation site"	2528	/note= "Casein kinase II phosphorylation site"	2936	/note= "Tyrosine kinase phosphorylation site"	5561	/note= "Tyrosine kinase phosphorylation site"	6971	/note= "Protein kinase C phosphorylation site"	7274	/note= "Protein kinase C phosphorylation site"	7376	/note= "cAMP and cGMP-dependent protein kinase	phosphorylation site"	7678	/note= "Protein kinase C phosphorylation site"	9496	/note= "Protein kinase C phosphorylation site"	97100	/note= "cAMP and cGMP-dependent protein kinase	phosphorylation site"	102105	/note= "Casein kinase II phosphorylation site"	128131	/note= "Casein kinase II phosphorylation site"	129, 153 /	/note= "Frotein Kinase Air-Dinding region signature"
Homo sapiens.	Key	Modified-site		Modified-site		Modified-site		Modified-site		Modified-site		Modified-site		Modified-site		Modified-site			Modified-site		Modified-site		Modified-site			Modified-site		Modified-site	;	binding-sice	
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"Protein kinase C phosphorylation site" "Casein kinase II phosphorylation site"

"Casein kinase II phosphorylation

"Protein kinase C phosphorylation site'

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"Asn is N-glycosylated" "N-myristoylation site"

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The invention relates to isolated human kinase proteins and nucleic acid and peptide sequences can be used as models for the development of human therapeutic targets, aid in the identification of therapeutic proteins and serve as targets for the development of human therapeutic agents that modulate kinase activity in cells and tissues therapeutic agents that modulate kinase activity in cells and tissues that express the kinase. The nucleic acids are useful as probes or primers, in constructing recombinant vectors, for expressing antigenic portions of the proteins, chromosome mapping, drug screening, testing an individual for a genotype, and for gene therapy in patients containing cells that are aberrant in kinase gene expression. The proteins may be used in drug screening assays, in the identification of compounds that modulate, stimulate or inhibit kinase activity, in pharmacogenomic modulate, in treating disorders characterised by an absence or unwanted expression of the protein (bone osteosarcoma, or colon-moderately differentiated adenocarcinoma), and in generating antibodies specific for the peptides. Such antibodies can be used to detect the protein in situ, in vitro, or in cell lysate or supernatant, to isolate and purify the proteins from host cells, pharmacogenomic analysis, tissue typing, and in thibiting protein function. The present sequence is human kinase protein gene is located on chromosome 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New human kinase proteins and nucleic acids, useful in drug screening assays, identifying modulators of kinase activity or treating disorders characterized by absence or unwanted expression of the protein.
                                                                                                   /note= "Serine/threonine protein kinase active-site
signature"
                                                                                                                                                                                                                                                                              324. .344

Anote= "Helix 1"

Anote= "Protein kinase C phosphorylation site"
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/note= "Protein kinase C phosphorylation site"
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19-MAR-2001; 2001US-00810671.
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/note= "F
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Beasley EM;

Di Francesco V,

Score 2410; DB 5; Length 445; Pred. No. 2.8e-221;

100.0%;

Best Local Similarity

Query Match

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PQHMIQKTRKRKYFHHNQLDWDEHSSAGRYVRRCKPLKEFMLCHDEEHEKLFDLVRRML 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunogen; STAT6 activation; allergy; inflammation; autoimmune disease; diabetes; hyperlipidaemia; infection; cancer; Th1 hyperactive disease; rheumatoid arthritis; osteoarthritis; systemic lupus erythematosus; sepsis; asthma; allergic rhinitis; ischaemic heart disease; subarachnoid haemorrhage; viral hepatitis; AIDS.
                                                                                             61 YRIHCSKSSVRSRRSSPKRKRNRHCSSHQSRSKSHRRKRSRSIEDDEEGHLICQSGDVLR
                                                                                                                                            1 MCIPLEASHSVEEDTHPSHYLEARSLNERDYRDRRYVDEYRNDYCEGYVPRHYHRDIESG
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2002JP-00377326.
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The invention relates to a purified protein promoting signal transducer and activator of transcription 6 activation (STAT6). The protein is useful for the producing an antibody, which involves administering the protein or its epitope-bearing fragments to a non-human animal as an antigen. The nucleic acid is useful for diagnosing a disease or susceptibility to a disease related to expression or activity of the protein. A transformant expressing the protein is useful for screening compounds which inhibit or promote STATE activation. A transformant expressing the protein is useful for producing a pharmaceutical composition. Compositions, antibodies and antisense molecules are useful for the treating a disease associated with STATE activation such as allergic diseases, inflammation, autoimmune diseases, diabetes, allerting disease associated with STATE activation and/or prevention of Thi hyperactive diseases. Compositions are also useful in rheumatoid attribing of observativity. The protein has efficient promoting STATE activation or inhibition of STATE. The present sequence represents the activation or inhibition of STATE. The promotein which promotes STATE activation. l transducer and activator of transcription 6 activation purified protein, for diagnosing and treating disease d with activation/inhibition of transcription factor e.g. Claim 1; SEQ ID NO 108; 1368pp; English. diabetes and cancer. signal associated promoting 

Sequence 481 AA;

116 212 236 272 296 DVLRARYEIVDTLGEGAFGKVVECIDHGMDGMHVAVKIVKNVGRYREAARSEIQVLEHLN 176 332 356 392 LGPIPQHMIQKTRKRKYFHHNQLDWDEHSSAGRYVRRRCKPLKEFMLCHDEEHEKLFDLV 416 93 IESGYRIHCSKSSVRSRRSSPKRKRNRHCSSHQSRSKSHRRKRSRSIEDDEEGHLICQSG 152 26 92 DVLRARYEIVDTLGEGAFGKVVECIDHGMDGMHVAVKIVKNVGRYREAARSEIQVLEHLN STDPNSVFRCVQMLEWFDHHGHVCIVFELLGLSTYDFIKENSFLPFQIDHIRQMAYQICQ SINFLHANKLTHTDLKPENILFVKSDYVVKYNSKMKRDERTLKNTDIKVVDFGSATYDDE HHSTLVSTRHYRAPEVILALGWSQPCDVWSIGCILIEYYLGFTVFQTHDSKEHLAMMERI SINFLHHNKLTHTDLKPENILFVKSDYVVKYNSKMKRDERTLKNTDIKVVDFGSATYDDE HHSTLVSTRHYRAPEVILALGWSQPCDVWSIGCILIEYYLGFTVFQTHDSKEHLAMMERI SHSSTQENRHCKPHHQFKESDCHYLEARSLNERDYRDRRYVDEYRNDYCEGYVPRHYHRD IESGYRIHCSKSSVRSRRSSPKRKRNRHCSSHQSRSKSHRRKRSRSIEDDEEGHLICQSG STDPNSVFRCVQMLEWFDHHGHVCIVFELLGLSTYDFIKENSFLPFQIDHIRQMAYQICQ 8 SH-SVEEDTH------PSHYLEARSLNERDYRDRRYVDEYRNDYCEGYVPRHYHRD Indels 11; Gaps 96.1%; Score 2315.5; DB 8; Length 481; 96.2%; Pred. No. 3.5e-212; ive 2; Mismatches 4; Indels 11; RRMLEYDPTQRITLDEALQHPFFDLLKKK 445 Query Match 96.1 Best Local Similarity 96.2 Matches 432; Conservative 213 417 153 117 177 297 333 393 237 357 33 273 453 셤 ద g 셤 Š ò ò 음 ò 셤 ò 셤 ò 8 ò

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The invention relates to a method of identifying compounds that influence fat cell number or size comprising providing a cell that expresses a gene and an agent, exposing the cell to the agent and identifying fat cell number or size relative to cells not exposed to the agent. The method also comprises providing an expression vector and an agent, exposing the cells not expression of the gene comprises providing a change in an expression of the gene relative to expression of the gene in an expression vector not exposed to the agent, treating a subject with the agent comprises an antisense oligonucleotide. The subject comprises an ammal, preferably a human. The method also comprises providing a polypeptide and an agent, exposing the polypeptide to the agent, detecting binding of the agent to the agent and identifying fat cell number or size in the subject. The agent comprises an antibody. A method of regulating fat cell number or size comprises providing a subject containing fat cells and an agent that changes the expression of a gene, and treating the subject with the agent under conditions so that fat cell size or number in the subject is altered. The method is useful for identifying compounds that influence fat cell number or size, for preparing a composition for treating or preventing obesity or diabetes. This sequence represents a human polypeptide used in the scope of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identifying compounds that influence fat cell number or size for treating or preventing obesity or diabetes by exposing the cell to the agent and identifying fat cell number or size relative to cells not exposed to the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 14; SEQ ID NO 352; 275pp; English.
                                                                                                                                                                                                                                                                                                                      09-OCT-2002; 2002US-00267502.
                                                                                                                                                                                                                                                                                                                                                           09-OCT-2002; 2002US-00267502.
                                                          01-JUL-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                   (LIFE-) LIFE SCI DEV CORP
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                                                                                             Human polypeptide #39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 481 AA;
                                                                                                                                                                                                                                       JS2004071700-A1
                                                                                                                                                          antidiabetic.
                                                                                                                                                                                                   Homo sapiens
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Best Local 8
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RESULT 3 ADO08026 ID ADO0

AD008026 standard; protein; 481 AA

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The invention relates to a novel isolated nucleic acid and the PRO polypeptide encoded by it. A protein of the invention has antiinflammatory, antiarthritic, antiinflammatory, antiarthritic, antiinflammatory, antiarthritic, antiporatic, immunosuppressive, osteopathic, antidiabetic, dermatological, antiporiatic, antialergic, antiasthmatic, hepatotropic, and respiratory activity. A polymucleotide of the invention may have a use in gene therapy. The PRO polypeptide, its agonist, antagonist, or antibody that specifically binds to the polypeptide is useful for treating an immune related disorder such as systemic lupus exythematosus, theumatoid arthritis, osteoarthritis, juvenile chronic arthritis, a spondylaarthropathy, systemic sclerosis, an idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
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                                                                                                                                                                                                                                                                                                                                                                               HHSTLVSTRHYRAPEVILALGWSQPCDVWSIGCILIEYYLGFTVFQTHDSKEHLAMMERI 392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive; osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic; antiasthmatic; hepatotropic; respiratory; gene therapy; immune system.
                                                                                                STDPNSVPRCVOMLEWFDHHGHVCIVPELLGLSTYDFIKENSFLPFOIDHIROMAYOICO
                                                                                                                                                                                                                                 SINFLHHNKLTHTDLKPENILFVKSDYVVKYNSKMKRDERTLKNTDIKVVDFGSATYDDE
                                                                                                                                                                                            SINFLHHNKLTHTDLKPENILFVKSDYVVKYNSKMKRDERTLKNTDIKVVDFGSATYDDE
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                                                              STDPNSVFRCVQMLEWFDHHGHVCIVFELLGLSTYDFIKENSFLPFQIDHIRQMAYQICQ
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thrombocytopenia, thyroiditis, diabetes meliitus, immune, mediated renal disease, a demyelinating disease of the central or peripheral nervous system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome, a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary disease, infectious or autoimmune chronic active hepatitis, primary billamatory bowel disease, gluen-sensitive enteropathy, Whitple's disease, an autoimmune or immune-mediated skin disease, a bullous skin disease, arythema multiforme, contact dermatitis, psoriasis, an allergic disease, asthma, allergic rhinitis, atopic dermatitis, food hypersensitivity, urticaria, an immunologic disease of the lung, contact premonia, idiopathic pulmonary fibrosis, hypersensitivity pneumonia, idiopathic pulmonary fibrosis, hypersensitivity pneumonia, idiopathic sequence represents a PRO protein or premonial contact disease, graff rejection or graff rejection or premonial contact disease, graff rejection or protein the present sequence represents a PRO protein
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vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
                                                                                                                                                                                                                                                                                                                                                                                   11;
                                                                                                                                                                                                                                                                                                                                               8; Length 481;
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Pred. No. 3.5e-212;
2; Mismatches 4;
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96.2%;
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Matches 432; Conservative
                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                            of the invention
                                                                                                                                                                                                                                                                                                              Sequence 481 AA;
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transcription 6; STAT6;

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immunogen; STAT6 activation; allergy; inflammation; autoimmune disease; diabetes; hyperlipidaemia; infection; cancer; Thi hyperactive disease; rheumatoid arthritis; osteoarthritis; systemic lupus erythematosus; sepsis; asthma; allergic rhinitis; ischaemic heart disease; subarachnoid haemorrhage; viral hepatitis; AIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                   New signal transducer and activator of transcription 6 activation promoting purified protein, for diagnosing and treating disease associated with activation/inhibition of transcription factor e.g.
             protein that promotes STAT6 activation #53.
                                       signal transducer and activator of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 106; 1368pp; English.
                                                                                                                                                                                                                                            06-JUN-2002; 2002US-0385912P.
26-DEC-2002; 2002JP-00377326.
27-DEC-2002; 2002JP-00137326.
15-MAY-2003; 2003JP-00137505.
16-MAY-2003; 2003US-0470836P.
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                                                                                                                                                                                                                                                                                                                            (ASAH ) ASAHI KASEI KK.
                                                                                                                                                                                                                                                                                                                                                                              WPI; 2004-122214/12.
N-PSDB; ADI26140.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            diabetes and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 481 AA;
                                                                                                                                                       WO2003104277-A2
                                                                                                                               sapiens
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DVLRARYEIVDTLGEGAFGKVVECIDHGMDGMHVAVKIVKNVGRYREAARSEIQVLEHLN 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DVLRARYEIVDTLGEGAFGKVVECIDHGMDGMHVAVKIVKNVGRYRVAARSEIQVLEHLN 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STDPNSVFRCVQMLEWFDHHGHVCIVFELLGLSTYDFIKENSFLPFQIDHIRQMAYQICQ 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SINFLHHNKLTHTDLKPENILFVKSDYVVKYNSKMKRDERTLKNTDIKVVDFGSATYDDE 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HHSTLVSTRHYRAPEVILALGWSQPCDVWSIGCILIEYYLGFTVFQTHDSKEHLAMMERI 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LGPIPOHMIOKTRKRKYFHHNOLDWDEHSSAGRYVRRRCKPLKEFMLCHDEEHEKLFDLV 416
                                                                                                                                                                                                                                                                                                                                                                                                                                               New cell cycle-regulating protein 53 and its polynucleotide, applicable in diagnosis and treatment of malignant tumor, hemopathy, human immundeficiency virus infection, immunological diseases and various
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STDPNSVFRCVQMLEWFDHHGHVCIVFELLGLSTYDFIKENSFLPFQIDHIRQMAYQICQ
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                                                                                                                                                                                                                                                          The present invention provides the protein and coding sequences for hu cell cycle regulating protein 53. The sequences can be used in the diagnosis and treatment of malignant tumours, haemopathy, human immunodeficiency virus (HIV) infection, immunological diseases and various types of inflammation. The present sequence is the cell cycle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                              4; Length 481;
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                                                                                                                                                                                                                                                                                                                                                                             Score 2294.5; DB 4;
Pred. No. 3.5e-210;
;; Mismatches 7;
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                                                                          (SHAN-) SHANGHAI BIO ROAD GENE DEV LID
                                                                                                                                                                                                                                   Claim 1; Page 23-24; 30pp; Chinese.
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                         16-OCT-2000; 2000WO-CN000328
                                                   99CN-00119816
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                                                                                                                                                                                                                                                                                                                                                                                         al Similarity 95.5
                                                                                                                                                                                                                                                                                                                            regulating protein 53
                                                                                                                               WPI; 2001-300480/31.
                                                                                                                                           N-PSDB; AAF89402.
                                                                                                                                                                                                                                                                                                                                                      Sequence 481 AA;
                                                                                                     Xie Y;
                                                   22-OCT-1999;
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Ishizawa K;

Muramatsu S,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   allergic diseases, inflammation, autoimmune diseases, diabetes, hyperlipidaemia, infections disease and cancers. Compositions are useful for treating disease associated with STATE activation and/or prevention of Thi hyperactive diseases. Compositions are also useful in rheumatoid arthritis, osteoarthritis, systemic lupus erythematosus, sepsis, asthma, allergic rhinitis, ischaemic heart diseases, subarachnoid haemorrhage, viral hepatitis and AIDS. The protein has efficient promoting STATE activity. The protein or nucleic acid is effectively useful for screening compounds for treating and preventing disease associated with excessive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57 IESGYRIHCSKSSVRSRRSSPKRKRNRHCSSHQSRSKSHRRKRSRSIEDDEEGHLICQSG 116
The invention relates to a purified protein promoting signal transducer and activator of transcription 6 activation (STAT6). The protein is useful for the producing an antibody, which involves administering the protein or its epitope-bearing fragments to a non-human animal as an antigen. The mucleic acid is useful for diagnosting a disease or susceptibility to a disease related to expression or activity of the protein. A transformant expressing the protein is useful for screening compounds which inhibit or promote STAT6 activation. A transformant expressing the protein is useful for screening composition. Compositions, antibodies and antisense molecules are useful for the treating a disease associated with STAT6 activation such as
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   compounds for treating and preventing disease associated with excessive activation or inhibition of STAT6. The present sequence represents the amino acid sequence of a human protein which promotes STAT6 activation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93.8%; Score 2261.5; DB 8 93.5%; Pred. No. 5.1e-207; ive 8; Mismatches 10;
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481

ADI26141 standard; protein;

(first entry)

22-APR-2004

ADI26141;

number or size in the subject. The agent comprises an antisense oligonuclectide. The subject comprises a mammal, preferably a human. The method also comprises providing a polypeptide and an agent, exposing the polypeptide to the agent, detecting binding of the agent to the polypeptide or a change in an activity of the polypeptide, treating a subject with the agent comprises an antibody. A method of regulating fat cell number or size comprises an antibody. A method of regulating fat cell number or size comprises providing a subject containing fat cells and an antibody. A method of regulating fat cell number or size comprises providing a subject containing the subject with the agent under conditions so that fat cell size or number in the subject is altered. The method is useful for identifying compounds that treating or preventing obsesty or size, for preparing a composition for treating or preventing obsesty or diabetes. This sequence represents a mouse polypeptide used in the scope of the invention.

Sequence 481 AA;

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Identifying compounds that influence fat cell number or size for treating or preventing obesity or diabetes by exposing the cell to the agent and identifying fat cell number or size relative to cells not exposed to the
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176
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                                                                                       STDPNSVFRCVQMLEWFDHHGHVCIVFELLGLSTYDFIKENSFLPFQIDHIRQMAYQICQ 272
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                                                                                                                                                                                                             HHSTLVSTRHYRAPEVILALGWSQPCDVWSIGCILIEYYLGFTVFQTHDSKEHLAMMERI 356
                                           DVLRARYEIVDTLGEGAFGKVVECIDHGMDGLHVAVKIVKONVGRYREAARSEIQVLEHLN
                                                                                                                  SINFLHHNKLTHTDLKPENILFVKSDYVVKYNSKMKRDERTLKNTDIKVVDFGSATYDDE
                                                                                                                             SINFLHINKLTHTDLKPENILFVKSDYVVKYNSKMKRDERTLKNTDIKVVDFGSATYDDE
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                                                                         STDPNSVFRCVQMLEWFDHHGHVCIVFELLGLSTYDFIXENSFLPFQIDHIRQMAYQICQ
                                                                                                                                                                                                                                                                                                                                                                                               Mouse, fat cell \mathsf{number}_j fat cell \mathsf{size}_j obesity; diabetes; anorectic; antidiabetic.
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N-PSDB; ADO07812.
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                                                                                                                                                57 IESGYRIHCSKSSVRSRRSSPKRKRNRHCSSHQSRSKSHRRKRSRSIEDDEEGHLICQSG
                                                                                                                SH-SVEEDTH------PSHYLEARSLNERDYRDRRYVDEYRNDYCEGYVPRHYHRD
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                                                            Gaps
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        DB 8; Length 481;
                                                         11; Indels
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Score 2252.5; DB 8;
Pred. No. 3.7e-206;
8; Mismatches 11;
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93.5%;
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                                                               Matches 419; Conservative
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159. .476
                                  Local Similarity
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        Query Match
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The invention relates to a method of identifying compounds that influence fat cell number or size comprising providing a cell that expresses a gene and an agent, exposing the cell to the agent and identifying fat cell number or size relative to cells not exposed to the agent. The method also comprises providing an expression vector and an agent, exposing the vector to the agent, detecting a change in expression of the gene relative to expression of the gene in an expression vector not exposed to the agent, treating a subject with the agent and identifying fat cell

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The present sequence is a novel protein kinase. The novel protein kinases and the nucleic acids that encode them may be used in the treatment and diagnosis of diseases associated with inappropriate kinase expression such as immune-related diseases and disorders, cardiovascular disease, neurodegenerative diseases and/or cancers. The nucleic acids and complementary sequences may also be used as DNA probes in diagnostic assays. The kinase polypeptides may be used as antigens in the production of antibodies of kinase expression and activity. Anti-kinase antibodies ant agonists may also be used to down regulate kinase expression and activity. Diseases related to kinase expression and activity include rheumatoid arthritis, atherosclerosis, autoimmune disorders, complications of organ transplantation, myocardial infarction, immune disorders, cardiomyopachies, strokes, renal failure, oxidative-stress related disorders, chronic inflammatory bowel disease, chronic
                                               391 LGPIPAHMIQKTRKRKYFHHNQLDWDEHSSAGRYVRRRCKPLKEFMLCHDEEHEKLFDLV 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human, mouse; protein kinase; antiarthritic; antisclerotic; osteopathic; immunosuppressive; cardiant; renal; antiinflammatory; antiasthmatic; dermatological; antidabetic; antiinfertility; gene therapy; vaccine; immune disorder; cardiovascular disease; neurodegenerative disease; cancer; autoimmune disorder; stroke; inflammatory bowel disease; inflammatory pelvic disease; multiple sclerosis; psoriasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                stress related disorders, chronic inflammatory bowel disease, chronic inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis, pecriasis, rhinitis, autoimmunity, diabetes, cancers and reproductive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids encoding kinase polypeptides, useful for diagnosing and treating immune-related diseases and disorders, cardiovascular disease, neurodegenerative diseases and/or cancers.
                       LGPIPQHMIQKTRKRKYFHHNQLDWDEHSSAGRYVRRRCKPLKEFMLCHDEEHEKLFDLV
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Pred. No. 3.5e-194;
2; Mismatches 5;
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                                                                                                              445
                                                                                                                                        RRMLEYDPTQRITLDEALQHPFFDLLKKK
                                                                                                                                                                                                                                                                                                                                                                                                          Novel protein kinase, SEQ ID NO: 175
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                                                                                                                                                                                                                                                                          AAB65648 standard; protein; 499
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Best Local Similarity 89.3
Matches 401; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI: 2001-032161/04.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAF44675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 499 AA;
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                                                                                                                                                                                                                                                                                                                                                                  27-MAR-2001
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                       357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This polypeptide comprises novel mouse CLK serine/threonine kinase mCLK4, from the CLK serine/threonine kinase family of proteins that regulate RNA splicing in cells. mCLK4 cDNA was cloned from a mouse embryo 11.5 p.c.
1ZAP CDNA library. The invention discloses the discovery of novel protein kinases mCLK2 (see AAW49912), mCLK3 and mCLK4 (see AAW49914) of mol.wt.
89.9, 58.5 and 57.2 kDa, respectively, as well as other novel proteins (see AAW49906-10) involved in cellular signal transduction, and provides vectors, host cells, purified recombinant proteins, methods for identifying compounds that activate or inhibit the novel proteins, as well as methods for the diagnosis and treatment of diseases associated with the novel proteins. Oversexpression of CLK serine/threonine kinases has been implicated in certain types of cancer. Compounds that inhibit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DVLRARYEIVDTLGEGAFGKVVECIDHGMDGMHVAVKIVKNVGRYREAARSEIQVLEHLN 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       212 STDPNSVFRCVQMLEWFDHHGHVCIVFELLGLSTYDFIKENSFLPFQIDHIRQMAYQICQ 271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DVLRARYEIVDTLGEGAFGKVVECIDHGMDGLHVAVKIVKNVGGYREAARSEIQVLEHLN 211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SINFLHHNKLTHTDLKPENILFVKSDYVVKYNSKMKRDERTLKNTDIKVVDFGSATYDDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  their catalytic activity or disrupt their interactions with natural binding partners may act as anti-cancer therapeutics. mCLK related molecules and compounds may also be useful as male contraceptives
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New phosphatase and kinase enzyme(s) - useful in the diagnosis and treatment of signal transduction disorders.
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Pred. No. 5.4e-199;
9; Mismatches 18; Indels 13;
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                                                                                                                                                                                                                                                                                                                                                                                                              Wang HY,
/note= "catalytic domain"
384. .389
/note= "LAMMER motif"
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96US-0023485P.
96US-0030860P.
96US-0030964P.
96US-0034286P.
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ses 409; Conserv
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15-NOV-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                            Ullrich
                       Peptide
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                     SHSSTQENRHCKPHHQFKESDCHYLEARSLNERDYRDRRYVDEYRNDYCEGYVPRHYHRD 140
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                                                                                                                                    STDPNSVFRCVQMLEWFDHHGHVCIVFELLGLSTXDFIKENSFLPFQIDHIRQMAYQICQ 290
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                                               IESGYRIHCSKSSVRSRRSSPKRKRNRHCSSHOSRSKSHRRKRSRSIEDDEEGHLICOSG 116
                                                                                    17 DVLRARYEIVDTLGEGAFGKVVECIDHGMDGMHVAVKIVKNVGRYREAARSEIQVLEHLN 176
                                                                                                     -----XEIVDTLGEGAFGKVVECIDHGMDGMHVAVKIVKNVGRYREAARSEIQVLEHLN 230
                                                                                                                                                                                  SINFLHHNKLTHTDLKPENILFVKSDYVVKYNSKMKRDERTLKNTDIKVVDFGSATYDDE 350
                                                                                                                                                                                                                                           LGPI PQHMIQKTRKRKY FHHNQLDWDEHSSAGRYVRRRCKPLKEFMLCHDEEHEKLFDLV 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New antisense compound targeted to a nucleic acid molecule encoding microtubule-affinity-regulating kinases (MARK3), useful for modulating expression of MARK3 or for treating cancer or Alzheimer's disease.
                                                                                                                                                                                                                HHSTLVSTRHYRAPEVILALGWSQPCDVWSIGCILIEYYLGFTVFQTHDSKEHLAMMERI
           ----PSHYLEARSLNERDYRDRRYVDEYRNDYCEGYVPRHYHRD
                                                                                                                          STDPNSVFRCVQMLEWFDHHGHVCIVFELLGLSTYDFIKENSFLPFQIDHIRQMAYQICQ
                                                                                                                                                                 SINFLHHNKLTHTDLKPENILFVKSDYVVKYNSKMKRDERTLKNTDIKVVDFGSATYDDE
                                                                                                                                                                                                     HHSTLVSTRHYRAPEVILALGWSQPCDVWSIGCILIEYYLGFTVFQTHDSKEHLAMMERI
                                                                                                                                                                                                                                                                                                                                                                                                                           Human, antisense gene therapy, MARK3;
MAP/microtubule affinity-regulating kinase 3; can be a selected and a selected.
Alzheimer's disease; neurodegenerative disorde;
                                                            141 IESGYRIHCSKSSVRSRRSSPKRKRNRHCSSHQSRS-
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           SH-SVEEDTH-
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base pairs (bp) targeted to a nucleic acid encoding MARK3 (MAP/microtubule affinity-regulating kinase 3), that specifically hybridises with the nucleic acid encoding MARK3 and inhibits expression of MARK3, i.e. is an antisense oligonucleotide (AO). Also included are a composition comprising the compound and a carrier or diluent, inhibiting the expression of MARK3 in cells or tissues, treating an animal having or suspected of having a disease or condition associated with MARK3 and screening for an antisense compound. The antisense oligonucleotide is useful for preparing a composition for treating hyperproliferative disorder, particularly cancer and neurodegenerative diseases e.g. Alzheimer's disease. The present sequence is a MARK3 associated protein included in the figures but not mentioned anywhere else in the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57 IESGYRIHCSKSSVRSRRSSPKRKRNRHCSSHQSRSKSHRRKRSRSIEDDEEGHLICQSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SINFLHHNKLTHTDLKPENILFVKSDYVVKYNSKMKRDERTLKNTDIKVVDFGSATYDDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SH-SVEEDTH------PSHYLEARSLNERDYRDRRYVDEYRNDYCEGYVPRHYHRD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STDPNSVPRCVQMLEWPDHHGHVCIVFELLGLSTYDFIKENSFLPFQIDHIRQMAYQICQ
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phosphate group; cancer; immune disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 2127.5; DB 8
Pred. No. 3.5e-194;
2; Mismatches 5;
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401; Conserv
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                                                                                                                                                                                                                                                                                                                                            specification.
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The invention provides human protein kinase molecules (HPKM) (AAY27052-57) and nucleic acid sequences (AAX89850-55) encoding the HPKM polypeptides respectively. The HPKM polypeptides can be produced recombinantly by standard recombinant methodology. Protein kinases add phosphate groups to proteins. HPKM polypeptide or an HPKM antagonist is
                                                                                                                                                                                                                                                                    /note= "potential signature sequence for protein kinase catalytic domain"
                                                                                                                                                                                                                                                                                                                                                     /note= "potential signature sequence for protein kinase
catalytic domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New human protein kinase molecules useful for treating or preventing cancer or an immune disorder.
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                                  'note= "potential phosphorylation site"
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                                                                                                        "potential
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Guegler KJ;
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242
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                                                                                                                                                                                        117 DVLRARYEIVDTLGEGAFGKVVECIDHGMDGMHVAVKIVKNVGRYREAARSEIQVLEHLN 176
                                                                                                                                                                                                      STDPNSVFRCVQMLEWFDHHGHVCIVFELLGLSTYDFIKENSFLPFQIDHIRQMAYQICQ 236
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                                                                                                                                                                                                                                                                                            HHSTLVSTRHYRAPEVILALGMSQPCDVWSIGCILJEYYLGPTVFQTHDSKEHLAMMERI 356
                                                                                                                                                                                                                                                                                                                                                                       LGPIPOHMIOKTRKRKYFHHNQLDWDEHSSAGRYVRRRCKPLKEFMLCHDEEHEKLPDLV 416
                                                                                                                                                                                                                                                                                                                                                                                   HHSTLVSTRHYRAPEVILALGWSQPCDVWSIGCILIEYYLGFTVFQTHDSKEHLAMMERI 362
                                                                                                                       92
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                                                                                                              || | :|: | CENTRECKPHHQFKESDCHYLEARSLNERDYRDYRDYVDEYRNDYCEGYVPRHYHRD
                                                                                                                                                                                                                                                 SIDPNSVPRCVQMLBWFDHHGHVCIVFELLGLSTYDFIKENSFLPFQIDHIRQMAYQICQ
                                                                                                  SH-SVEEDTH------PSHYLEARSLNERDYRDRRYVDEYRNDYCEGYVPRHYHRD
                                                                                                                                                          SINFLHHNKLTHTDLKPENILFVKSDYVVKYNSKMKRDERTLKNTDIKVVDFGSATYDDE
                                                                             Gaps
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used to treat or prevent cancer or an immune disorder. The present sequence represents the amino acid sequence of {\sf HPKM-3}
                                                                           41;
                                                      Length 451;
                                                                           6; Indels
                                                     DB 2;
                                                     Score 2117.5; DB 2
Pred. No. 2.7e-193;
3; Mismatches 6;
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                                                        87.9%;
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                                                      Query Match
Best Local Similarity 88.9
Matches 399; Conservative
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N-PSDB; ADO07810.
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                                 Sequence 451 AA;
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Page 10

or preventing obesity or diabetes by exposing the cell to the agent and identifying fat cell number or size relative to cells not exposed to the

Claim 14; SEQ ID NO 353; 275pp; English.

The invention relates to a method of identifying compounds that influence fat cell number or size comprising providing a cell that expresses a gene and an agent, exposing the cell to the agent and identifying fat cell number or size relative to cells not exposed to the agent. The method also comprises providing an expression vector and an agent, exposing the vector to the agent detecting a change in expression of the gene relative to expression of the gene in an expression vector not exposed to the agent, treating a subject. The agent comprises an antisense relative to expression of the subject. The agent comprises an antisense oligonucleotide. The subject with the agent comprises an antisense oligonucleotide to the agent, detecting binding of the agent to the agent, exposing the polypeptide to the agent, detecting binding of the agent to the agent comprises an antibody. A method of regulating fat cell subject with the agent comprises an antibody. A method of regulating fat cell number or size comprises providing a subject containing fat cells and an agent that changes the expression of a gene, and treating the subject with the agent under conditions so that fat cell size or number in the subject is altered. The method is useful for identifying compounds that influence fat cell number or size, for preparing a composition for treating or preventing obesity or diabetes. This sequence represents a human polypeptide used in the scope of the invention.

Sequence 484 AA;

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255
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                                                                                                                                                                                                                                                                                                             78.5%; Score 1893; DB 8; 82.3%; Pred. No. 8.9e-172; ive 30; Mismatches 44;
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Matches 353; Conservative
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(first entry) 09-APR-2002 Serine and Threonine protein kinase Clk.

MAPKAP-K3; AP-3 delta; APP-695; amyloid A4; Hsp8; heat shock protein 8; Li30; NY-REN-58; P38 Alpha; P38 Beta; ERK3; KIAA0934; CDK9; coell cycle dependent kinase 9; CLK; C-MAPL-1; clathrin heavy chain; amphiphysin; PN9109; KIAA1106; neurodegenerative disorder; non-insulin dependent diabetes mellitus; NIDDM; Alzheimer's disease; inflammatory disease; rheumatold arthritis; inflammatory bowel disorder; atherosclerosis; cardiac hypertrophy; hypoxic brain injury; yeast two-hybrid; signal transduction pathway; human; mitogen activated protein kinase.

Homo sapiens

Region

Location/Qualifiers
1. .364
forte= "This region binds the mitogen activated protein kinase (MAPK) ERK3 (see AAU75105), the bait protein in yeast two-hybrid assay, producing a complex claimed in claim 1"

W0200198524-A2

27-DEC-2001.

21-JUN-2001; 2001WO-US019762

22-JUN-2000; 2000US-0213245P

(MYRI-) MYRIAD GENETICS INC.

Heichman K, Bartel PL;

WPI; 2002-122287/16.

New protein complexes comprising protein-protein interactions (e.g. MAPKAP-K3/AP-3 delta or C-NAP-1/Clathrin HC), useful for diagnosing physiological generative disorders or screening drugs for these diseases. 

Example 9; Page; 60pp; English

The invention describes an isolated protein complex, comprising two proteins. The protein complex comprises: protein kinase MAPRAP-K3 and APD-CC 3 adaptor complex delta sub-unit; MAPKAP-K3 and amyloid A4 precursor. Protein, APP-695; MAPKAP-K3 and heat shock protein kinase ERK3 and call cycle dependent kinase (CDK) 9 (IAAN0934 (unknown function); ERK3 and cell cycle dependent kinase (CDK) 9; ERK3 and protein kinase (CDK) 9; ERK3 and interactions. The protein complexes are useful for diagnosing physiological generative disorders, drug screening for agents that modulate the interaction of the proteins (thus identify drug targets), and identifying additional proteins in the pathway common to the proteins. These physiological disorders include non-insulin dependent disabetes mellitus (NIDDM), neurodegenerative disorders (e.g. rheumatory bowel disorder) and other human disease such as atherosclerosis, cardiac hypertrophy and hypoxic brain injury. This sequence represents the serine and threenine kinase Clk, residues 1-364 of which binds to the bait protein ERK3, a mitogen activated protein kinase (AAU75105) in a yeast two-hybrid assay for determining components of signal transduction pathways and forms an interaction claimed in claime continuation. Note: This sequence does not appear in the components of the invention. Note: This sequence does not appear in the components of such as a pecification but has been obtained from a reference given in the

Sequence 484 AA;

Length 484; Score 1887; DB 5; Pred. No. 3.3e-171; 78.3%; Best Local Similarity Query Match

AAU75108 standard; protein; 484 AA. AAU75108 RESULT 13 AAU75108 ID AAU7 XX AC AAU7

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ADR14001 standard; protein; 484 AA
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                                                                 Sequence 484 AA;
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Matches 352
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                                                         KVVECIDHGMDGMHVAVKIVKNVGRYREAARSEIQVLEHLNSTDPNSVFRCVQMLEWFDH 195
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                                                                                                                HGHVCIVPELLGLSTYDFIKENSFLPFQIDHIRQMAYQICQSINFLHHNKLTHTDLKPEN 255
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                                                                                                                                                1LFVKSDYVVKYNSKMKRDERTLKNTDIKVVDFGSATYDDEHHSTLVSTRHYRAPEVILA 315
                                                                                                                                                          LGWSQPCDVWSIGCILIEYYLGFTVPQTHDSKEHLAMMERILGPIPQHMIQKTRKKYFH 375
                                                                                                                                                                                           HNQLDWDEHSSAGRYVRRRCKPLKEFMLCHDEEHEKLFDLVRRMLEYDPTQRITLDEALQ 435
                                                                                                                                                                                                                          77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention comprises antisense oligonucleotides that are targeted to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New antisense oligonucleotides targeted to nucleic acid molecules encoding CDC-like kinase 1, useful for treating diseases or conditions associated with expression of CDC-like kinase 1, e.g. cancers or
                                                                                                                         HGHICIVPELLGLSTYDFIKENGFLPFRLDHIRKMAYQICKSVNFLHSNKLTHTDLKPEN
                                                                                                                                                                                                                                                                                                                                                                          antisense oligonucleotide, CDC-like kinase 1; cancer;
autoimmune disorder; infection; inflammation; tumour formation; human.
                                                                                          KVVECIDHKAGGRHVAVKIVKNVDRYCEAARSEIQVLEHLNTTDPNSTFRCVQMLEWFEH
                SHYLEARSLNERDYRDRRYVDEYRNDYCEGYVPRHYHRDIESGYRIHCSKSSVRSRRSSP
Gaps
7
Indels
45;
Mismatches
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                                                                                                                                                                                                                                                                                                                                                          Human CDC-like kinase-1 protein #1.
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                                                                                                                                                                                                                                                                                                          ADH58849 standard; protein; 484
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N-PSDB; ADH58708,
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aberrant acute phase response; hypercongenital condition; birth defect;
necrotic lesion; wound; organ transplant rejection;
aberrant signal transduction; proliferating disorder; cancer;
CDC-like kinase 1. The antisense oligonucleotides of the invention are useful for modulating the expression of CDC-like kinase 1, and for treating diseases or conditions associated with expression of CDC-like kinase 1 (e.g. cancers and autoimmune disorders). The antisense oligonucleotides may also be used to prevent or delay infection, inflammation and tumour formation. The present amino acid sequence represents a human CDC-like kinase 1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HGHICIVFELLGESTYDFIKENGFLPFRLDHIRKMAYOICKSVNFLHSNKLTHTDLKPEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           5;
                                                                                                                                                                                                                                                                                                                                                                                 Length 484;
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                                                                                                                                                                                                                                                                                                                                                                             tch 78.3%; Score 1887; DB 8; al Similarity 82.1%; Pred. No. 3.3e-171; 352; Conservative 30; Mismatches 45;
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HIV propagation; human.

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This invention relates to the novel association of protein sequences (and the genes which encode them) to the NF-kappaB pathway. The invention may be useful for the production of compounds with an anticinilammatory, cycostatic, hepatotropic, virucide, antiarthritic, anticinilammatory, cycostatic, hepatotropic, virucide, antiarteriosclerotic, anticinilammatory, cycostatic, nepatotropic, virucide, antiarteriosclerotic, manipuscupressive or immunodulator, cerebroprotective, vasotropic, immunosuppressive or vulnerary activity or for gene therapy. The proteins and nucleotides are useful for diagnosing, preventing, treating, or ameliorating conditions or diseases associated with the NF-kappaB pathway. The condition is an immune disorder; an inflammatory disorder, an inflammatory disorder, an inflammatory disorder, an inflammatory disorder, and inflammatory disorders, hoggkin's lymphomas, N=minked anhidrotic crodermal dysplasia, X-linked anhidrotic crodermal dysplasia, immunodeficiency, viral infections, HV-1, HTLV-1, crodermal dysplasia, immunodeficiency, viral infections, HV-1, HTLV-1, crodermal dysplasia, immunodeficiency, viral infections, enthyroid sick survival; evasion of immune responses, rheumatoid arthritis, inflammatory bowel disease, colitis, asthma, atherosclerosis, cachexia, euthyroid sick organ transplant rejection, conditions related to oberrant adult transplant rejection, conditions related to oberrant signal transplant croderion, conditions related to oberrant signal transplant croderion, conditions percent sequence is that of a human protein which the rivinses. The present sequence is that of a human protein with the NP-kappaB pathway of the invention. Note: This sequence does not appear in the provel sesociation with the NP-kappaB pathway of the rovel sesoc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated polynucleotides and polypeptides associated with NF-kappaB pathway, useful for diagnosing, treating, or preventing disorders or diseases associated with NF-kappaB pathway.
                                                                                                                                                                                                                                                                                                                                                                                   Carman J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 2; 237pp; English
                                                                                                                                                                                                                                                                                                                                                                                Neubauer MG, Feder JN,
                                                                                                                                                                                                                                                                                                                            (BRIM ) BRISTOL-MYERS SQUIBB CO.
                                                                                                                                                                                                                                                   14-JAN-2003; 2003US-0440068P.
12-MAY-2003; 2003US-0469757P.
                                                                                                                                                                                                   13-JAN-2004; 2004WO-US000798.
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                                                                                                WO2004065577-A2
                                                    Homo sapiens.
                                                                                                                                                  05-AUG-2004
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114 KSKARIHHSTSHRRSHGKSHRRKRTRSVEDDEEGHLICQSGDVLSARYELVDTLGEGAFG 173
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                                                                                                                                                                                                                                                                                                                                      174 KVVECIDHKAGGRHVAVKIVKNVDRYCEAARSEIQVLEHLNTTDPNSTFRCVQMLEWFEH 233
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                                                                                                 18 SHYLEARSLNERDYRDRRYVDEYRNDYCEGYVPRHYHRDIESGYRIHCSKSSVRSRRSSP
                                                                                                                          SHYLESRSINEKDYHSRRYIDEYRNDYTQGCEPGHRQRDHESRYQNHSSKSSGRSSY
                                                 2;
78.3%; Score 1887; DB 8; Length 484; 82.1%; Pred. No. 3.3e-171; ive 30; Mismatches 45; Indels 7
                        Best Local Similarity 82.1
Matches 352; Conservative
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HGHVCIVFELLGLSTYDFIKENSFLPFQIDHIRQMAYQICQSINFLHHNKLTHTDLKPEN 255

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HGHICIVFELLGESTYDFIXENGFLPFRLDHIRXMAYQICKSVNFLHSNKLTHTDLKPEN 293
                                                    316 LGWSQPCDVWSIGCILIEYYLGFTVPQTHDSKEHLANMAERILGPIPQHMIQKTRKRKYFH 375
                                       ILFVKSDYVVKYNSKMKRDERTLKNTDIKVVDFGSATYDDEHHSTLVSTRHYRAPEVILA 315
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US-05-810-671-1

Sequence 1, Application US/09810671

Sequence 1, Application No. US20020076783A1

Sequence 1, Application No. US20020076783A1

GENERAL INFORMATION:

APPLICANT: YAN, Chunhua et al

TITLE OF INVENTION: ACID MCLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: US/09/810,671

CURRENT FILING DATE: 2001-06-08

NUMBER OF SEQ ID NOS: 5

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1

LENGTH: 2354
                            Sequence 3, Appli Sequence 3, Appli Sequence 136, Appli Sequence 136, Appli Sequence 113, Appli Sequence 113, Appli Sequence 113, Appli Sequence 121, Appli Sequence 121, Appli Sequence 22, Appli Sequence 22, Appli Sequence 22, Appli Sequence 24, Appli Sequence 131, Appli Sequence 24, Appli Sequence 24, Appli Sequence 133, Appli Sequence 133, Appli Sequence 133, Appli Sequence 24, Appli Sequence 133, Appli Sequence 134, Appli Sequence 134, Appli Sequence 134, Appli Sequence 134, Appli Sequence 135, Appli Sequence 135, Appli Sequence 256, Appli Sequence 256, Appli Sequence 256, Appli Sequence 5456, A
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3 US-10-109-854-3

5 US-10-339-656-3

8 US-10-425-3

7 US-10-425-114-26212

7 US-10-154-708-3

8 US-10-267-502-136

7 US-10-267-502-140

7 US-10-267-502-140

10-10-267-502-140

10-10-267-502-140

10-10-267-502-140

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US-10-267-502-137
US-10-367-502-134
US-10-367-720-1439
US-10-108-260A-2256
US-10-104-047-656
US-10-425-114-16170
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US-10-057-475B-5456
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100.0%; Pred. No. 0;
Live 0; Mismatches
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Best Local Similarity 100.
Matches 2256; Conservative
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ORGANISM: Human
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| Cgn2_6/ptodata/2/pubpna/USO6_PUBM_PUB.seq:*
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| Cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
| Cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
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GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

FILE REFERENCE: CLOOO758DIN US/10/109,854

CURRENT APPLICATION NUMBER: US/10/109,854

CURRENT FILING DATE: 2002-04-01

PRIOR APPLICATION NUMBER: 09/810,671

PRIOR FILING DATE: 2000-08-24

PRIOR FILING DATE: 2001-03-19

NUMBER OF SEQ ID NOS: 5

SOFTWARE: FastSEC for Windows Version 4.0
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100.0%; Score 2256;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2256; Conservative 0; Mismatches
                                                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Homo sapien
US-10-109-854-1
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1812   TARATITIAAGITGITAITCITITICATGGGTGATGAAAACCAGACATTC   1931	RESULT 5 US-10-425-114-26852 i 95-10-425-114-26852 j Sequence 26852, Application US/10425114 j Publication No. US20040034888A1 j GENERAL INFORMATION: j APPLICANT: Liu, Jingdong APPLICANT: Screen, Steven E APPLICANT: Screen, Steven E APPLICANT: Tabaska, Jack E APPLICANT: Tabaska, Jack E APPLICANT: TILE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53313)B CURRENT FILING DATE: 2003-04-28 NUMBER OF SEQ ID NOS: 73128 SEQ ID NO 26852 LENGTH: 4035 TYPE: DNA ORGANISM: Homo sapiens FRATURE:	0uery Match         84.6%; Score 1908.4; DB 17; Length 4035;           Best Local Similarity         99.3%; Pred. No. 0;           Matches 1909; Conservative         0; Mismatches         1; Indels         0; Gaps         0;           Oy         327 ATATCHARATCGTGGACACTTTGGGTGAAGGTGCTTTGGCAAGTTGTAGAGTGCATTGA         386         0;           Oy         312 AGATGAAATCGTGGACACTTTGGGTGAAAATCGTAAAAATGTAGGTGCATTGA         2185           Oy         387 TCATGGCATGGATGCATGTAGAAGTGAAAATCGTAAAAAATGTAGGCGTTACCG         2245           Db         2186 TCATGGCATGGATGCATGTAAAAAAAAAAAAAAAAAAAA
	1201 GACCTGGTTCGAAGAATGTTAGAATATGATCCAACTCAAAGAATTACCTTGGATGAAGCA 1260  1272 GACCTGGTTCGAAGAATGTTAGAATATGATCCAACTCAAAGAATTACCTTGGATGAAGCA 1310  1261 TTGCAGCTCCTTTCTTTGACTTATTAAAAAGAATGAATGGGAATCAGTGGTCTTAC 1320  1322 TTGCAGCATCCTTTCTTTGACTTATTAAAAAGAATGAAATGGGAATCAGTGGTCTTAC 1391  1324 TATATACTTCTCTTGACTTATTAAAAAAAAAAAAAAAAA	ATAAATGGGATTGATCTTTGTACATGGGGGCACCTCTGAAGTGATTTTTTTT

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                                                                                                                                                                                                                                                                                                                                                         THE DETECTION
                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC
                                                                                                                                                                                       RESUL: ,
US-10-641-643-699
US-10-641-643-699
US-10-641-643-699, Application US/10641643
; Publication No. US20040077003A1
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; Suban G. Stuart
; Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; SEQUENCE DESCRIPTION; SEQ ID NO: 699 : US-10-641-643-699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                  TCTTTGACTTATTAAAAAAAATGA 1299
                                                                                                         STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
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TELEPHONE: (650) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1456 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (650) 845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 699
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
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Best Local Similarity
Matches 1191; Conserv
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                       AAAGCGGGTATCGAATCCACTGCAGTAAATCTTCAGTCCGCAGCAGGAGAAGCAGTCCTA
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: ULLAICH, Axel

APPLICANT: ULLAICH, Axel

TITLE OF INVENTION: CLK PROTEIN KINASES AND RELATED PRODUCTS AND METH

FILE REFERENCE: 036602/0431

CURRENT PILLING DATE: 2010.07-17

PRIOR APPLICATION NUMBER: 09/127,248

PRIOR APPLICATION NUMBER: 09/127,248

PRIOR APPLICATION NUMBER: 09/127,248

PRIOR APPLICATION NUMBER: 09/127,248

PRIOR APPLICATION NUMBER: 09/127,286

PRIOR PILLING DATE: 1997-06-17

PRIOR PILLING DATE: 1997-06-17

PRIOR APPLICATION NUMBER: US 60/034,286

PRIOR FILLING DATE: 1997-06-17

PRIOR PILLING DATE: 1996-12-19

PRIOR PILLING DATE: 1996-12-19

PRIOR PILLING DATE: 1996-12-19

SEQ ID NOS: 26

LEMANTH: 1549

TWO DEL TOWN THE PRIOR DATE: 2000-11 PRIOR PILLING DATE: 1996-12-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1549;
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Pred. No. 1.4e-220;
0; Mismatches 121; Indels
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Best Local Similarity 90.6%;
Matches 1170; Conservative
                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
CRGANISM: Mus musculus
US-09-905-999-26
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> RESULT 8 US-09-905-999-26 ; Sequence 26, Application US/09905999

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Query Match
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Publication No. US20040259220A1

GENERAL INFORMATION:

APPLICANT: ULLRICH, Axel

APPLICANT: ULLRICH, Axel

APPLICANT: ULLRICH, Axel

TITLE OF INVENTION: CLK PROTEIN KINASES AND RELATED PRODUCTS AND METHODS

FILE REPERENCE: 038602/0431

CURRENT APPLICATION NUMBER: US/10/825,177

CURRENT PILING DATE: 2001-04-16

PRIOR APPLICATION NUMBER: 09/127,248

PRIOR FILING DATE: 1999-07-31

PRIOR FILING DATE: 1999-07-31

PRIOR FILING DATE: 1997-06-17

PRIOR PRIOR APPLICATION NUMBER: US 60/034,286

PRIOR PRIOR DATE: 1997-06-17

PRIOR FILING DATE: 1997-06-17

PRIOR FILING DATE: 1997-06-17

PRIOR FILING DATE: 1997-06-17

PRIOR APPLICATION NUMBER: US 60/034,286

PRIOR APPLICATION NUMBER: US 60/034,286
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                                                                                                  74 ACGAATACAGGAATGACTGTGTGAAGGATATGTTCCTAGACATTATCACAGAGACATTG
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                                                                           GTCATTATTTAGAAGCAAGGTCCTTGAATGAGCGAGATTATCGGGACCGGAGATACGTTG
                                        Gaps
     DB 18; Length 1549;
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48.6%; Score 1097.4; DB 1.
90.6%; Pred. No. 1.4e-220;
iive 0; Mismatches 121;
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                                                CTGACCCCAACAGTGTTTCCGATGCGTCCAGATGCTAGAGTGGTTTGATCATGATGTC
                                                                                                                                                            GCTTTCTGCCATTTCAAATTGACCACATCAGGCAGATGGCGTATCAGATCTGCCAGTCAA
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Publication No. US2020076783A1
GENERAL INFORMATION: US2020076783A1
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS,
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLO00758
CURRENT APPLICATION NUMBER: US/09/810,671
CURRENT FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PASTSEQ for Windows Version 4.0
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TGAAGGAATTTATGCTTTGTCATGATGAGAACATGAGAAACTGTTTGACCTGGTTCGAA
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                                                                                                                                                                         GAATGTTAGAATATGATCCAACTCAAAGAATTACCTTGGATGAAGCATTGCAGCATCCTT
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                                                AGCTAGATTGGGATGAACACAGTTCTGCTGGTAGATATGTTAGGAGACGCTGCAAACCGT
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48.6%; Score 1097.2; DB 17; Lengt
Best Local Similarity 90.8%; Pred. No. 1.5e-220;
Matches 1168; Conservative 0; Mismatches 118; Indels
                                                                                                                                                                                                                                                     TCTTTGACTTATTAAAAAGAAATGAAATGG 1304
                                                                                                                                                                                                                                                                                                                                       Sequence 138, Application US/10267502
Publication No. US20040071700A1
GENERAL INFORMATION:
APPLICANT: Kim, Jaeseob
TITLE OF INVENTION: Obesity Linked Genes
TITLE OF INVENTION: Obesity Linked Genes
CURRENT APPLICATION NUMBER: US/10/267,502
CURRENT FILING DATE: 2003-01-27
NUMBER OF SEQ ID NOS: 439
SEQ ID NO 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Mus musculus
US-10-267-502-138
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US-10-267-502-138
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Sequence 3, Application US/10109854
; Sequence 3, Application US/20020119548A1
; General INFORMATION:
    General INFORMATION:
    APPLICANT: YAN, Chunhua et al.
    TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
    TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
    TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
    TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
    TITLE OF INVENTION WOMBER: US/10/109,854
    CURRENT FILING DATE: 2002-04-01
    PRIOR FILING DATE: 2000-08-24
    PRIOR FILING DATE: 2001-03-19
    NUMBER OF SEQ ID NOS: 5
    SOFTWARE: FastSEQ for Windows Version 4.0
    SEQ ID NO 3
    LENGTH: 21234
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                                                                                                                                                           TYPE: DNA
CORGANISM: Homo sapien
US-10-109-854-3
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                                                                                             Length 21234;
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48.6%; Score 1097; DB 9;
Best Local Similarity 100.0%; Pred. No. 6e-220;
Matches 1097; Conservative 0; Mismatches 0;
; SEQ ID NO 3
; LENGTH: 21234
; TYPE: DNA
; ORGANISM: Human
US-09-810-671-3
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18558 TIGCCTTTIGTACATGGAGGTCACCTCTGAAGTGATTTTTTTGAGTAAAAGGAAATCTT
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                                                  1157 AGGAATTTATGCTTTGTCATGAAGAACATGAGAAACTGTTTGACCTGGTTCGAAGAA
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Best Local Similarity 100.0%; Pred. No. 6e-220; Matches 1097; Conservative 0; Mismatches 0;
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US-10-339-656-3
i Sequence 3, Application US/10339656
i Publication No. US20030134319A1
i GENERAL INFORMATION:
I GENERAL INFORMATION:
I TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
I TITLE OF INVENTION: THEREOF
I PRIOR APPLICATION NUMBER: 09/810,671
I PRIOR PILING DATE: 2000-08-24
INVENTIOR PILING DATE: 2000-08-24
I NUMBER OF SEQ ID NOS: 5
I SEQ ID NO 3
I TITLE OF INVENTION: THEREOF
I TITLE OF INVENTION: THEREOF
I TITLE OF INVENTION: THE TITLE OF THE TITLE
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                                    8618 GACTACTITATATITCTIAAAGGAAATATITCTITATATACTITCAAAITITAGAACTITA
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; ORGANISM: Homo sapien
US-10-339-656-3
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US-10-425-114-26212

Sequence 26212, Application US/10425114

Sequence 26212, Application Wo. US2004003488841

Sequence 26212, Application No. US2004003488841

APPLICANT: Liu, Jingdong

APPLICANT: Liu, Jingdong

APPLICANT: Abou, Yihua

APPLICANT: Ace, Youngwei

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: Nucleic Acid Molecules Associated With

TITLE OF INVENTION: NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NO 26212

LENGTH: 3040
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Pred. No. 3.5e-195;
0; Mismatches 1;
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US-10-425-114-26212
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Best Local Similarity 99.9%;
Matches 978; Conservative (
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| Sequence 3, Application US/2080152123A1
| Publication No. US20040152123A1
| GENERAL INFORMATION:
| APPLICANT: YAN, Chunhua et al.
| TITLE OF INVENTION: ISCLATED HUMAN KINASE PROTEINS, NUCLEIC
| TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
| TITLE OF INVENTION: THEREOF
| TITLE OF INVENTION: US/10/801,671
| CURRENT FILING DATE: 2004-03-17
| PRIOR PELLING DATE: 2004-03-17
| PRIOR APPLICATION NUMBER: 09/810,671
| PRIOR APPLICATION NUMBER: 09/810,671
| PRIOR PILING DATE: 2000-08-24
| PRIOR FILING DATE: 2001-03-19
| NUMBER OF SEQ ID NOS: 5
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO
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ö 660 720 131 311 300 371 431 420 491 480 551 540 611 600 671 731 191 9 GENERAL INFORMATION:

GENERAL INFORMATION:

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TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND

TITLE OF INVENTION: THEREOF

FILE REFERENCE: CLOOO758DIV-III

CURRENT FILING DATE: 2004-03-17

FRIOR PILING DATE: 2004-03-17

FRIOR PILING DATE: 2001-03-19

NUMBER OF SEQ ID NOS: 5

SOPTWARE: FESTER OF LOW WINDOWS: 5

SEC ID NOS: 5

SEC ID NOS: 5 GACACTCATCCCCAGTCATTATTTAGAAGCAAGGTCCTTGAATGAGCGAGATTATCGGGAC CGGAGATACGTIGACGAATACAGGAATGACTACTGTGAAGGATATGTTCCTAGACATTAT AGCCACCGAAGGAAAAAATCCAGGAGTATAGAGGATGATGAGGAGGGTCACCTGATCTGT ATCTGCCAGTCAATAAATTTTTACATCATAATAAATTAACCCATACAGATCTGAAGCCT GACACTCATCCCAGTCATTATTTAGAAGCAAGGTCCTTGAATGAGCGAGATTATCGGGAC CGGAGATACGTTGACGAATACAGGAATGACTACTGTGAAGGATATGTTCCTAGACATAT AGAAGCAGTCCTAAAAGGAAGCGCAATAGACACTGTTCAAGTCATCAGTCACGTTCGAAG AGCCACCGAAGGAAAGATCCAGGAGTATAGAGGATGATGAGGAGGGTCACCTGATCTGT CAAAGTGGAGACGTTCTAAGAGCAAGATATGAAATCGTGGACACTTTGGGTGAAGGAGCC CAAAGTGGAGACGTTCTAAGAGCAAGATATGAAATCGTGGACACTTTGGGTGAAGGAGCC TITGGCAAAGTIGIAGAGTGCATTGATCATGGCATGGATGGCATGCATGTAGCAGTGAAA **ATCGTAAAAATGTAGGCCGTTACCGTGAAGCAGCTCGTTCAGAAATCCAAAGTATTAGAG** CACTTAAATAGTACTGATCCCAATAGTGTCTTCCGATGTGTCCAGATGCTAGAATGGTTT GATCATCATGGTCATGTTTTGTGTTTTGAACTACTGGGACTTAGTACTTACGATTTC Length 2354; 0; Indels DB 63; 100.0%; Score 2256; 100.0%; Pred. No. 0; iive 0; Mismatches Conservative TYPE: DNA
CORGANISM: Homo sapiens
US-10-801-671-1 Query Match Best Local Similarity Matches 2256; Conserv LENGTH: 2354 241 432 552 181 312 541 601 661 -72 132 252 301 372 361 481 612 61 121 192 421

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Sequence 1, Application US/10111076A

GENERAL INFORMATION:
APPLICANT: MAO, Yumin
APPLICANT: MIE, YI
TITLE OF INVENTION: A NEW POLYPEPTIDE - NEW CELL CYCLE-REGULATIING PROTEIN 53 AND 11 TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING THE SAME
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING THE SAME
CURRENT APPLICATION NUMBER: POLYNUCLEOTIDE ENCODING THE SAME
CURRENT APPLICATION NUMBER: POLYNUCLEOTION PRICE 2002-04-19
PRIOR APPLICATION NUMBER: PCT/CN/00328
PRIOR FILING DATE: 2000-10-16
PRIOR FILING DATE: 2000-10-16
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 1.
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ORGANISM: Homo sapiens
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; Pred. No. 0;
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GENERAL INFORMATION:
APPLICANT: PLOWMAN, GREGORY D.
APPLICANT: MARTINEZ, RICARDO
APPLICANT: WHYTE, DAVID
APPLICANT: WHYTE, DAVID
APPLICANT: SUDERSANAM, SUCHA
TITLE OF INVENTION: PROTEIN KINASES
FILE REFERENCE: 038602/1273
CURRENT APPLICATION NUMBER: US/09/979,167
CURRENT FILING DATE: 2001-11-20
NUMBER OF SEQ ID NOS: 269
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 55
LENGTH: 2488
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Best Local Similarity 95.9%;
Matches 2148; Conservative (
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i_LOCATION: (562)
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## APPLICANT: Diep, Dinh  ### TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using  ### TITLE OF INVENTION: Polymucleotide Sequence Databases, and Single Nucleotide  ### TITLE OF INVENTION: Polymorphisms Identified Thereby  ### TITLE REFERENCE: 62.0010-1 P.  ### CURRENT APPLICATION NUMBER: US/60/278,258  ### CURRENT FILING DATE: 2001-03-23  ### NUMBER OF SEQ ID NOS: 17730  ### SOGTWARE: PERL Program  ### SEQ ID NO 3721  ### SEQ ID NO 3721  ### PRESTURE:  ### ORGANISM: Home sapiens  ### FEATURE:  ### ORGANISM: INFORMATION: Incyte ID No: 253847.3  US-60-278-258-3721	Query Match 90.7%; Score 2047; DB 97; Length 2487; Best Local Similarity 95.9%; Pred. No. 0; Matches 2148; Conservative 0; Mismatches 0; Indels 91; Gaps 1;  Qy 14 GTCATTATTAGAAGCAAGGTCCTTGAATGAGGGAATTATGGGGACCGGAGATACGTTG 73  Dh 3.98 GTCATTATTAGAAGCAAGGTCCTTGAATGAGGGAATTATCGGGACCAGAATACGTTG 73  Dh 3.98 GTCATTATTAGAAGCAAGATCCTTGAATGAGGAATTATCGGAATACGTTG 73	74 ACGAATACAGGAATGACTACTGTGAAGGATATGTTCCTAGACATTATCACAGAGACATTG 	Qy 134 AAAGCGGGTATCGAATCCACTGCAGTAAATCTTCAGTCCGCAGCAGGAGAAGCAGTCCTA 193	Qy 194 AAAGGAAGGCAATAGACACTGTTCAAGTCATCAGTCGAAGAGCCACCGAAGGA 253	Qy 254 AAAGATCCAGGAGTATAGAGGATGATGAGGGTCACCTGATCTGTCAAAGTGGAGACG 313  Db 562 561	Qy         314 TTCTAAGAGCAAGATATGAAATCGTGGACACTTTGGGTGAAGGGCTTTGGCAAAGTTG         373           Db         562ATGAAATCGTGGACACTTTGGGTGAAGGAGCCTTTGGCAAAGTTG         606	Qy 374 TAGAGTGCATTGATCATGGCATGGATGCATGTAGCAGTGAAATCGTAAAAAATG 433	Oy 434 TAGGCCGTTACCGTGAAGCAGCTCGTTCAGAAATCCAAGTATTAGAGCACTTAAATACTA 493	Oy 494 CTGATCCCAAIAGTGTCTTCCGATGTGTCCAGAIGCTAGAAIGGTTTGATCATCAIGGTC 553	Qy 554 ATGTTTGTATTGTGTTTGACTACGGACTTACGATTTCATTAAGAAAACA 613	Qy         614 GCTTTCTGCCATTTCAAATTGACCACATGGCGAGATGGCGTATCAGATCTGCCAGTCAA         673           Db         847 GCTTTCTGCCATTTCAAATTGACCACATCAGGCGAATGGCGTATCAGATCTGCCAGTCAA         906	Oy 674 TABATTITTACATCATAAATTAACCCATACAGATCTGAAGCCTGAAATATTITGT 733	Oy 734 TIGTGAAGTCTGACTATGTAGTCAAATATAATTCTAAAATGAAACGTGATGAACGCACAC 793
1463 TCTTGACTTATTAAAAAGAAATGAAATGGGAATCAGTGGTCTTACTATATACTTCTCT 1522 1334 AGAAGAGATTACTTAAGACTGTGTCAGTCAAACATTCTAATATTTTGTAAACATT 1393 1523 AGAAGAGATTACTTAAGACTGTGTCAACTAAACATTCTATATTTTTGTAAACATT 1582 1394 AAATTATTTTGTACAGTTAAGTGTAAATATTTTGTATCAATAGTTTTTGTAACATT 1582 1583 AAATTATTTTGTACAGTTAAGTGTAAATTTTTGTATCAATAGTAATTAAC 1453 1484 TTGTTAAGCAAGTAACGTTAAAATGCATTAGAAAATTAAATTATTTTTTTT	1574 AICTIGCCTITIGIACAIGGAGGICACCTCTGAAGIGAITITITITIAGIAAAAGGAAAT 1633 	1694 TITAAAAGTITTTCTTCTGTAATTGTTGAACGGGTGATTATTATTAACTCTAGATAAGCA T1883 TITAAAAGTTTTTCTTCTGTAATTGTTGAACGGGTGATTATTATTAACTCTAGATAAGCA 1883 TITAAAAAGTTTTTCTTTCTGTAATTGTTGAACGGGTGATTATTAACTCTAGATAAGCA	1754	1814 TIGIAITCITITICAITGGGIGAIGICAGGGIGAIAACCAGACAITCAIGGAAAGGCAIG 1873 	1874 CAGITIGICCAITGIGACAGITIGITITAAIAAACCACAIACACATTIAITITAAGAITA 1933 	1934 AAAICTAACTGGAAAGTCAGCTTGGAAAATGGACATTTCCAAGTATGTTTGGTGAGTCAC 1993 2123 AAATCTAACTGGAAAGTCAGCTTGGAAAATGGACATTTCCAAGTATGTTTGGTGAGTCAC 2182	1994 AGHTATAAAATHGGAAATTCTGATGAGAGGTTTCAGTTTTTAATACCAAGTCCTTAGGAG 2053 	2054 TCTTAACATTGGCCAGCATCTGTTATCAAATGACATAAATACGTAAACCTATAAGAATT 2113 	2114 AAGTTTATTAATTAGCCAATTTATGTCTGTGATAATTCTTACGGGGAAGAGGATTTGA 2173 	2174 TTGGAAAGCAGTTTGGGAAQAAAGTGCTGCTGAATTTCCAGAATTTAATTGATTGGTTA 2233 	2234 CATAAACTTTTGACTTCA 2252 	SULT 5 -60-278-258-3721 Sequence 3721, Application US/60278258	
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STRANDEDNESS: single TOPOLOGY: linear IMMEDIATE SOURCE: LIBRARY: NEUTFWT01 CLONE: 339963 SEQUENCE DESCRIPTION: SEQ ID NO: 9:	tch al 214	GTCATTATTAGAAGGTCCTTGAATGAGCGAGATATCGGGACCGGAGATACGTTG  [	348 ACGAGIACAGGAGIGACIACIGICAAGGATAIGITCCIAGACAITATCACAGAGACAITG 407 134 AAAGGGGGTATCGAATCCACTGCAGTAAATCTTCAGTCCGCAGCAGAGAAGCAGTCCTA 193 11	194 AAAGGAAGCGCAATAGACACTGTTCAAGTCATCAGTCACGTTCGAAGAGCCCCGAAGGA 253	314. TICTAAGAGCAAGATATGAAATCGTGGACACTTTGGGTGAAGGAGCCTTTGGCAAAGTTG 373	TAGAGTGCATTGATCATGCATGGATGGCATGCATGTAGCATGAAAGAAA	434 TAGGCCGTTACCGTGAAGCAGCTCGTTCAGAAATCCAAGTATTAGAGCACTTAAATTAGTA 493 	494 CTGATCCCAATAGTGTCTCCAGATGCTAGAATGGTTTGATCATCATGGTC 553 	554 AIGTITGIAITGIGIIIGAACIACIGGGACTIAGIACITACGAITTCAITAAAGAAACA 613 	614 GCTITCTGCCATTTCAAATTGACCACATCAGGCAGATGGCGTATCAGATCTGCCAGTCAA 673 	674 TAAATITTTTACATCATAAATTAACCCATACAGATCTGAAGCCTGAAAATATTTGT 733 	734 TIGIGAAGICIGACTAIGIAGICAAATATATTCTAAAATGAAACGTGATGAAGGCACAC 793 	794 TGAAAAACACAGATATCAAAGTTGTTGACTTTGGAAGTGCAACGTATGATGATGATGATGACTC 853 	

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aagittattattaattaggcaatttatgtctgtgataattcttacgggggagaagaggattga 2173 	δ, qq	807 TATCAAAGTIGTIGACTITIGGAAGIGCAACGIATGAIGAACATCACAGTACTITIGGT 866 
tiggaaaggagtiigggaagaagigctgctgaaatiiccagaatitaaitgatigatia 2233 	co qa	867 GTCTACCGGGCACTACAGAGCTCCCGAGGTCATTTTGGCTTTAGGTTGGTCTCAGCCTTG 926
CATAAACTTTTTGACTTCAGAAA 2256 	\$ qa	927 TGATGTTTGGAGCATAGGTTGCATTCTTATTGAATATTACCTTGGTTTCACAGTCTTTCA 986
	රු යි	987 GACTCATGATAGTAAGAGCACCTGGCAATGATGGAACGAATATTAGGACCCATACCACA 1046 
oplication N: Tingdong Yihua	රු යු	1047 ACACATGATTCAGAAAACAGAAAAGCCAAGTATTTTCACCATAACCAGCTAGATTGGGA 1106 
, David K. Steven E Jack E ngwei	යි යි	1107 TGAACACAGTICTGCTGGTAGATATGTTAGGAGACGCTGCAAACCGTTGAAGGAATTTAT 1166
OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With OF INVENTION: Plants and Uses Thereof for Plant Improvement REFERENCE: 38-21(53313) B NT APPLICATION NUMBER: US/10/425,114	\$ Q	1167 GCTTTGTCATGATGAAGAACATGAGAAACTGTTTGACCTGGTTCGAAGAATGTTAGAATA 1226 
CURRENT FILING DATE: 2003-04-28 NUMBER OF SEQ ID NOS: 73128 SEQ ID NO 26852 LENGTH: 4035	y da	1227 IGATCCAACTCAAAGAATTACCTTGGAAGCATTGCAGCATCCTTTCTTT
TYPE: DNA ORGANISM: Homo sapiens FEATURE: OTHER INFORMATION: CLone ID: LIB4654-056-G4_FLI	vo ob	1287 AAAAAAGAAATGAAATGGGAATCAGTGGTCTTACTATACTTCTCTAGAAGAGATTACT 1346 
6%; Score 1908.4; DB 54; Length 4035; 9%; Pred, No. 0;	S G	1347 TAAGACHGTGTCAGTCAACTAAACATTCTAATATTTTGTAAACATTAAATTATTTGTA 1406 
); Conservative 0; Mismarches 1; Indels 0; Gaps 0; ATATGAAATCGTGGACACTTTGGGTGAAGGGCCTTTGGCAAAGTTGTAGAGGGCCTTTGG 386	<b>7</b> 60 00	
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OTHER INFORMATION: Similar to gi2645856 in the genepept database release 115,
OTHER INFORMATION: Run with FASTXY 3.3t00, default parameters
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                                                                                                   APPLICANT: Tang, Y. Tom
APPLICANT: Tillinghast, John
APPLICANT: Sinku, Ankura
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Novel Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 792
CURRENT FAPLICATION NUMBER: US/09/577,408
CURRENT FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 8502
SOFTWARE: PL GCT_genes Version 1.0
SEQ ID NO 3087
LENGTH: 2494
                                                                        Sequence 3087, Application US/09577408 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
                                              RESULT 10
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Qy         1274 TCTTGACTTATTAAAAAGAAATGAAATGGGAATCAGTGGTCTTACTATATATA	RESULT 12  US-10-932-349-580  Sequence 580, Application US/10932349  Sequence 580, Application US/10932349  GENERAL INFORMATION:  APPLICANT: CARGILL, Michele  TITLE OF INVENTION: BOCYDING HUMAN KINASE PROTEINS, METHODS OF DETECTION AND  TITLE OF INVENTION: USES THEREOF  TITLE OF INVENTION: USES THEREOF  TITLE OF INVENTION: USES THEREOF  CURRENT APPLICATION NUMBER: US/10/932,349  CURRENT FILING DATE: 2004-09-02  NUMBER OF SEQ ID NOS: 123188  SOUTHWARE: FastSEQ for Windows Version 4.0  SEQ ID NO 580  LENGTH: 1795  TYPE: DNA  ORGANISM: Homo sapiens  US-10-932-349-580	Query Match         72.5%;         Score 1634.6;         DB 65;         Length 1795;           Best Local Similarity 99.9%;         Pred. No. 0;         0;         10 Gaps         0;           Matches 1634;         Conservative 1;         Mismatches 0;         10 Gaps         0;           Qy         14 GTCATTATTAGAGGAAGGTCCTTGAATGAGGAGATTATCGGGACCGGAGATACGTTG         220           Db         16.1 GTCATTATTAGAAGGAAGGTCCTTGAAGGATTATCGGGACCAGAGATAGGTTG         220           Qy         74 ACGAATACAGGAATGACTACTGGAAGGATATCTCCTAGACTATATCAGAGACATTG         280           Qy         134 AAAGGAGGAATCGAACTACTGCAGAGATATCTCAGACAGA
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Db 1541 AAATTATTTGTACAGTTAAGTGTAAATATTGTATGTATCAATAGCATAATTAAC 1600  Qy 1454 TTGTTAAGCAAGTATGGTCTTGATAATGCATTAGAAAATTAAATTTTTTTT	RESULT 13 US-60-500-337-580  j Sequence 580, Application US/60500337  j GENERAL INFORMATION:    APPLICANT: CARGILL, Michele    TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES    TITLE OF INVENTION: DICTOR HUMAN KINASE PROTEINS, METHODS OF DETECTION AND    TITLE OF INVENTION: USES THEREOF    TITLE OF INVENTION: USES THEREOF    TITLE OF INVENTION: USES THEREOF    CURRENT APPLICATION NUMBER: US/60/500,337    CURRENT APPLICATION NUMBER: US/60/500,337    CURRENT PILING DATE: 2003-09-05    NUMBER OF SEQ ID NOS: 123188    SOFTWARE: FeatSEQ for Windows Version 4.0    SEQ ID NO 580    LENGTH: 1795    TYPE: DNA    ORGANISM: Homo sapiens    US-60-500-337-580	
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US-10-756-149-49

US-10-756-149-49

Sequence 49, Application US/10756149

SEQUENCE 41: Natasha

APPLICANT: Aziz, Natasha

APPLICANT: Aziz, Natasha

TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS NOVEL REPRESENCE: file

FILE REPRESENCE: file

CURRENT APPLICATION NUMBER: US/10/756,149

CURRENT APPLICATION NUMBER: US/10/756,149

CURRENT FILING DATE: 2004-01-12

NUMBER OF SEQ ID NOS: 5818

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LENGTH: 1814
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Sequence 338, Application US/60474733

GENERAL INFORMATION:
APPLICANT: The Procter & Gamble Company
APPLICANT: Infort, Mobert J.
TITLE OF INVENTION: Methods for Identifying Compounds for Regulating Muscle Mass of TITLE OF INVENTION: Punction
TITLE OF INVENTION: Punction
TITLE OF INVENTION: Punction
TITLE OF INVENTION NUMBER: US/60/474,733
CURRENT APPLICATION NUMBER: US/60/474,733
CURRENT FILING DATE: 2003-05-30
NUMBER OF SEQ ID NOS: 353
SOFTWARE: PatentIn version 3.2
SEQ ID NO 338
LENGTH: 1814
TYPE: DNA
ORGANISM: Homo sapiens
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| LOCATION: (1562)..(1562)
| OTHER INFORMATION: n is a,
| US-60-474-733-338
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Best Local Similarity 99.3
Matches 1638; Conservative
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GenCore version 5.1.6  Copyright (c) 1993 - 2005 Compugen Ltd.  OM nucleic - nucleic search, using sw model  Run on:  March 16, 2005, 07:34:52 ; Search time 7297.99 Seconds (without alignments)  11766.665 Million cell updates/sec  Title:  VS-10-801-671-1_COPY_72_2327  Perfect score: 2256 Sequence:  1 gacactcatcccagtcattaaaactttttgacttcagaaa 2256 Scoring table: IDBNTITY NUC Gapop 10.0 , Gapext 1.0  Searched:  34239544 seqs, 19032134700 residues  Total number of hits satisfying chosen parameters: 68479088	Minimum DB seq length: 0 Maximum DB seq length: 2000000000  Post-processing: Minimum Match 0% Maximum Match 100%	first (13: * * * * * * * * * * * * * * * * * * *	No. is greater s derive	1   1644.4   72.9   2798   3   CR749504   Homo sapi

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

In (Dases 1 to 1556)

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.L., Wang, J., Haieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McKernan, R.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
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/db_xref="C1:51476701"
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      TTCTAAGAGCAAGATATGAAATCGTGGACACTTTGGGTGAAGGAGCCTTTTGGCAAAGTTG
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                                                                    AAAGATCCAGGAGTATAGAGGATGATGAGGAGGGTCACCTGATCTGTCAAAGTGGAGACG
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Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalon,D.K., Muzny,D.M., Sodergren,B.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakeeley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Procc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Brin Garland, Ran Guin, Letticia Heiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duanes Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 15 Row: d Column: 16 series: selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 10190705 This clone has the following problem: frame shifted.
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                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (15-OCT-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTCATTATTTAGAAGCAAGGTCCTTGAATGAGCGAGATTATCGGGACCGGAGATACGTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: MGC help desk
Email: cgapbs-remail.nin.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
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Pred. No. 2e-265;
0; Mismatches 3; Indels 0;
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/clone lib="NH MGC 71"
/lab host="DH10B" -
/note="Vector: pCMV-SPORT6"
                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH-MGC Project URL: http://mgc.nci.nih.gov
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/db_xref="taxon:9606"
/clone="IMAGE:3908500"
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Matches 1285; Conservative
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAAGGAAGCGCAATAGACACTGTTCAAGTCATCAGTCACGTTCGAAGAGCCACCGAAGGA 253
                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1416)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanembaum, D.M., Civello, D.R., Lu, F., Murphy, B., Perriera, S., Wanoy, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA This sequence was made by sequencing genomic exons and ordering them based on alignment.
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                                                                                                                                                                                                                                                                                                                                                                 2 (bases 1 to 1446)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Givello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Direct Submission
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                                                                  Homo sapiens CLK4 gene, VIRTUAL TRANSCRIPT, partial genomic survey sequence.
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      1529 TCTTTGACTTATTAAAAAAAAAAAAAA 1556
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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/locus_tag="HCM3162"
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Mus musculus 13 days embryo head cDNA, RIKEN full-length enriched
library, clone:3110002D09 product:CDC like kinase 4, full insert
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                          1085 CTACAAGACATTATAGAGCACCCTGAAGTTATTTAGCCCTAGGGTGGTCGTCCCAGCCTTGTG
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Mus musculus (house mouse)
Mus musculus
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KSSGRSGRSGYRSKHRIHHSTSHRRSHGDEIVDTLGEGAFGKVVECIDHKAGGRHVAV
KIVKNVDKYCEAARSEIQVLEHLMYTOPNSTFRCVOMLEWEEHIGHICTVFELIGLST
YDFIKENGFLEFRLINDIIRKMAYQICKSVNFLHSNKLTHTDLKPENILFVQSDYTEAYN
PKIKRDERTLINDDIKVVDFGSATYDDEHFSTLVSTHIYRAPEVILFALGWSQPGTWAS
IGGILMEYYLGFTVRQTHDSKEHLAMMERILGPIPQHINIQKTRKKYFHHNOLDWDEH
SSAGRYVRRRCKPLKEFMLCHDEEHEKLFDLVRRMLEYDPTQRITLDBALQHPFPDLL
KKK"
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/db_xref="GI:9437515"
/trānslation="MRHSKRTYCPDWDDKDWDYGKWRSSSSHKRRKRSHSSAQENKRC
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 1865)

                                                                                                           2 (bases 1 to 1865)
Diaco, Li,N., Peng,Y., Han,Z. and Chen,Z.
Direct Submission
Submitted (08-DEC-1999) Chinese National Human Genome Center at
Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong,
Shanghai 201203, People's Republic of China
Location/Qualifiers
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Pred. No. 5.1e-230;
0; Mismatches 129; Indels 0;
                                                      Han, Z. and
                                                  Zhao, M., Song, H., Li, N., Peng, Y., Han, Z. an A novel gene expressed in human bone marrow Unpublished
                                                                                                                                                                                                                                                                                                                     /tissue type="bone marrow"
154. .1515
/codon_start=1
/product="CLK4"
                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/trānslation="MOGLHVAVKIVKNVGRYREAARSEIQVLEHLNSTDPNSVFRCVQ
MLEMFDLHGGIVCIVFELLGLSTYDFTKENSFLDFRQIDHIRWAYQICQSINFLHHWKL
THDLKKENILPVKSDPVKNNSKMREDERTLKNYDIKVVDFGSATYDDEHHSTLVST
RHYKAPEVILALGWSQPCDVWSIGGILIEYYLGFTVPQTHDSKGHLAMMERILGSPIPA
HMIQKTRKRKYFHHNQLDWDBHSSAGRYVRRCKPLKEFMLCHDEEHBKLFDLVRRML
                                                                                                                                           enriched mouse cDNA library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               253 AAAAGATCCAGGAGTATAGAGGATGATGAGGAGGGTCACCTGATCTGTCAAAGTGGAGAC 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84 AGTCACTATTTAGAAGCAAGATGCTTGAATGAGAGAGTTATCGGGACCGGAGATACATT
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                                                                                                                                                                                                                                                    Anote="unnamed protein product; CDC like kinase 4 (MGD|MGI:1098551, GB|NM_007714, evidence: BLASTN, 99%,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGTCATTATTTAGAAGCAAAGGTCCTTGAATGAGCGAGATTATCGGGACCGGAGATACGTT
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Pred. No. 2.7e-221;
0; Mismatches 183; Indels 103;
/db_xref="FANTOM_DB:3110002D09"
/db_xref="taxon:10090"
/clone="3110002D09"
                                                                                                                                                  /clone lib="RIKEN full-length
                                                                                                                                                                         dev stage="13 days embryo
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/proteIn_id="BAC25420.1"
/db_xref="G1:26379558"
                                                                                                                tissue_type="head"
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On Dec 10, 2002 this sequence version replaced gi:12851571.
Pleage visit our web site (http://genome.gsc.riken.jp/) for further
                                                                                                                                                                                                                                                                                                                            Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, M., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Pujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 1629)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Adachi, J., Alzawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Hrangaki, T., Hara, A., Hayateu, N., Hiramcto, K., Hiraoka, T., Hori, F., Imotani, K., Ishi, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Osaito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Yoshino, M., Muramatsu, M. and Hayashizaki, Y., Yoshida, K., Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The RIKEN Genome Exploration Research Group Phase II Team and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The FANTOM Consortium and the RIKEN Genome Exploration Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FANTOM Consortium. Functional annotation of a full-length mouse cDNA collection
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/strain="C57BL/6J"
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Direct Submission

L. Submission

L. Submission

L. Submission

L. Submission

Rockville, MD 20850, USA

This sequence was made by sequencing genomic exons and ordering them based on alignment.

Location/Qualifiers

1. 1421

| A. 1421
| Mol_type="genomic DNA"
| Mol_xref="taxon:10090"
                         Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
1 (Dases 1 to 1421)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Pertiera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
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                musculus (house mouse)
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KEYWORDS
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                                            Gaps
                                          25;
      Length 1421;
Score 978.2; DB 9; Length
Pred. No. 9e-200;
0; Mismatches 180; Indels
    Query Match
Best Local Similarity 84.1%;
Matches 1081; Conservative
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GSS 15-DEC-2003 sequence,

AY408254 110 DNA linear Mus musculus CLK4 gene, VIRTUAL TRANSCRIPT, partial genomic survey sequence.

AY408254 AY408254.1 GI:39764225

DEFINITION ACCESSION VERSION

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                                           Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
Direct Submitsed on Cargill, M.
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Sockville, MD 20850, USA
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
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Pred. No. 4.9e-191;
0; Mismatches 346;
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Science 302 (5652), 1960-1963 (2003)
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/locus_tag="HCM3162"
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Best Local Similarity 73.1%;
Matches 940; Conservative (
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pan troglodytes CLK4 gene, VIRTUAL TRANSCRIPT, partial sequence,
AX408253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1154 TGAAGGAATTTATGCTTTGTCATGAAGAACATGAGAACTGTTTGACCTGGTTCGAA 1213
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Clark, A.G. Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adans, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1094 AGCTAGATTGGGATGAACACAGTTCTGCTGGTAGATATGTTAGGACACGCTGCAAACCGT
                                                               701 ATGTTTGTATTGTGTTTGAGCTGGGACTTAGTACCTATGATTTTATTAAAGAAATA
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                                                                                                                                   GCTTTCTGCCATTTCAAATTGACCACATCAGGCAGATGGCGTATCAGATCTGCCAGTCAA
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                                                                                                                                                                 TCTTTGACTTATTAAAAAAAATGA 1299
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                                                                                                                                                                                                                                                                  13 AGTCATTATTTAGAAGCAAGGTCCTTGAATGAGCGAGATTATCGGGACCGGAGATACGTT
                                                                                                                                                                                                                                                                                                    238 AGCCATTATTTGGAAAGCAGGTCTATAAATGAGAAAGATTATCATAGTCGACGCTACATT
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                                                                                                                                                                              36.1%; Score 814.8; DB 3;
73.4%; Pred. No. 1.4e-164;
tive 0; Mismatches 382;
            /organism="Homo sapiens"
mol_type="mRNA"
db_xref="taxon:9606"
/clone="CLOBA009ZE09"
/tissue_type="Placenta"
/plasmid="pCMVSPORT_6"
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Matches 1102; Conservative
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Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

Location/Qualifiers
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full-length cDNA clone CL0BA009ZE09 of Placenta of Homo sapiens
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Pull-length cDNA libraries and normalization
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CR591789.1 GI:50472596
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Homo sapiens (human)
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was normalized. Library was constructed by Life Technologies, division of Invitrogen.
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                                                                                                                                                                                                          Score 814.8; DB 3;
Pred. No. 1.4e-164;
0; Mismatches 382;
                                Location/Qualifiers
1. 1746
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSOBF036YH24"
/tissue_type="Petal"brain"
/plasmid="pcMvSpORT_6"
                                                                                                                                                                                                            Query Match 36.1%;
Best Local Similarity 73.4%;
Matches 1102; Conservative
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1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
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                     CATAACCAGCTAGATTGGGATGAACACAGTTCTGCTGGTAGATATGTTAGGAGACGCTGC 1146
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full-length cDNA clone CS0DF036YH24 of Petal brain of Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1746)
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                                                                        CTTGGTTTCACAGTCTTTCAGACTCATGATAGTAAAGAGCACCTGGCAATGATGGAACGA
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http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue
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CR612115.1 GI:50492922
CR612115.1 GI:50492922
HTC; CNSLT cDNA.
Homo sapiens (human)
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us-10-801-671-1\_copy\_72\_2327.rst

COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pcMvSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.  FEATURES  1. 1754  Cource //organism="MRNA"  //db xref="taxon:9606" //db xref="taxon:9606" //clone="CSODIO367H19" //tissue type="Placenta Cot 25-normalized" //plasmid="pcMvSPORT_6"	Query Match     36.1%; Score 814.8; DB 3; Length 1754;       Best Local Similarity 73.4%; Pred. No. 1.4e-164;       Matches 1102; Conservative 0; Mismatches 382; Indels 18; Gaps 4;       Qy     13 AGTCATTATTAGAAGCAAGGTCCTTGAATCAGCAGATTATCGGGACGGAGATACGT 72       Db     238 AGCCATTATTTGGAAAGCAAGGTCTATAAATCAGAAAGATTATCATAGTCGACGCTACATT 297	Qy         73 GACGAATACAGGAATGACTACTGTGAAGGATATGTTCCTAGACATTATCACAGAGACATT 132           Db         298 GATGAGTACAGAATGACTACACTCCAAGGATGTGAACCTGGACATCGCCAAGAGACCAT 357           Qy         133 GAAAGCGGGTATCGAATCCACTGGAGAAATCTTCAGTCCGCAGCAGAAGAGACAGTCT 192           Db         358 GAAAGCGGATACAGAACCATAGTAGTAGCAAGTCTTCTGGTAGAAGTGGAAGATAGTTAT 417           Qy         193 AAAAGGAACCATAGAAGCCAATAGTAGCAAGTCTTCTGGTAGAAGTGGAAGAGCCAC 246           Qy         193 AAAAGGAAGCAATAGAACATAGTAGCAAGTCATCAAGTCACCATCGAAGAGCCAC 246	247 CGAAGGAAAGATCCAGAGTATAGAGGATGATGAGAGGGTCACCTGATAGAGAGAG	427 AANAATGTAGGCCGTTACCGTGAAGCAGCTCGTTCAGAAATCCAAGTATTAGAGCACTTA	Oy 607 GAAACAGCTTTCTGCCATTTCAAATTGACCACATCAGGCGTATCAGATCTGC 666
	Qy         1087 CATAACCAGCTAGATTGGGATGAACACAGTTCTGCTGGTAGATATGTTAGGAGGCTGC 1146           Db         1317 CACGATCGATTAGACTGGAGGTTCTGGCGGCAGATATGTTTCAAGACGTGT 1376           Qy         1147 AAACCGTTGAAGGAATTTATGCTTTGTCATGATGAAGAACATGAGAAACTTTGACCTG 1206           Db         1377 AAACCTCTAGAGAAATTTATGCTTTCTCAAGATGTTGAACATGAGGGGTCTCTTTGACCTC 1436	1207 GTTCGAAGAATGTTAGAATATGATCCAACTCAAAGAATTACCTTGGATGAAGCATTGCAG   126   12	Oy 1385 GTAAACATTAATTTTGTACAGTTAAGTTTTGTATGTTTTGTATGTTTTTTTT	1754 k iens (human). GI:50498279 CDNA. 8 (human) Metazoa; Chordata;	Primates; Catarrhini; Hominidae; Homo. Jussee, J. and Polayes, D. oraries and normalization  3 Email: fliang@lifetech.com URL: nvitrogen.com/ InVitroGen Corporation 16  004) Genoscope - Centre National de Sequedex - FRANCE (E-mail: segref@genoscope

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Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM14086 row m column: 21
High quality sequence stop: 587.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1207 GTTCGAAGAATGTTAGAATATGATCCAACTCAAAGAATTACCTTGGATGAAGCATTGCAG 1266
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           CGCACCTTAATAAATCCAGATATTAAAGTTGTAGACTTTGGTAGTGCAACATATGATGAC 1077
                                                                                            1198 ciriciscrirracceraririccaacacacaradraagaagaacarriaccaargaragaaaga 1257
                                                                  906
                                                                                                                                                                          907 TIAGGIIGGICTCAGCCTIGIGAIGITIGGAGCAIAGGIIGCAITCTIAITGAAIAIIAC 966
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 973)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1549 GCTCTCTCGAAGAGA-TCTTACAGACTGTATCAGTCTAATTTTTAAATTTTAAGTTATTT
                                                                  GAACATCACAGTACTTTGGTGTGTTTACCCGGCACTACAGAGCTCCCGAGGTCATTTTGGCT
                                                                                                                                                                                                                                                                                                                                                                                                       ATATTAGGACCCATACCACACACATGATTCAGAAAACAAGAAAACGCAAGTATTTTCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1438 ATTCAGAAAATGTTGGAGTATGATCCAGCCAAAAGAATTACTCTCAGAGAAGCCTTAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. David Rowe
CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          973 bp mRNA linear ES:
AGENCOURT 10105484 NIH_MGC_134 Mus musculus cDNA clone
IMAGE:6513308 5', mRNA sequence.
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Mus musculus
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LOCUS
DEFINITION
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Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishi, Y., Ltoh, M., Kagwa, T., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Nach, H., Nomura, K., Nomusaki, R., Ohno, M., Ohsato, N., Okazaki, K., Nomis, K., Nomusaki, R., Ohno, M., Ohsato, N., Sanci, R., Saitch, R., Saitch, R., Sakai, K., Sakai, K., Saitch, R., Sakai, C., Sakai, K., Sakai, K., Saitch, R., Saitch, R., Sakai, C., Sakai, K., Sakai, K., Saitch, R., Saitch, H., Sakai, K., Sakai, K., Saitch, R., Sa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tissue type="placenta and extra embryonic tissue" /clone lib="RIKEN full-length enriched mouse cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ä
                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Ranagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72 TGACGAATACAGGAATGACTACTGTGAAGGATATGTTCCTAGACATTATCACAGAGACAT 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGAAAGCGGGTATCGAATCCACTGCAGTAAATCTTCAGTCCGCAGCAGGAGGAGGAGTCC 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Rike Genomic Science Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="PROTEIN KINASE CLK1 (EC 2.7.1.-) (CLK) (PROTEIN KINASE STY) homolog [Mus musculus] (SWISSPROT | P22518, evidence: FASTY, 95%ID, 100%length, match=1449)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             440 acaaadraaacacadagagacgccaccaccaccaccaccaccaccatrcacacggaagagacca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  192 TAAAAGGAAAGCGCAATAG-----ACACTGTTCAAGTCATCAGTCACGTTCGAAGAGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.2 CAGTCATTATTTAGAAGCAAGGTCCTTGAATGAGCGAGATTATCGGGACCGGAGATACGT
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Pred. No. 3.1e-147;
0; Mismatches 324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM_DB:3830430K12"
/db_xref="raxon:1009"
/clone="3830430K12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/
Location/Qualifiers
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Matches 957
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                                                                                                           1246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of eap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
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                                                                                                                                                                                                                                       1306 AATCAGTGGTCTTACTATATACTTCTCT-AGAAGAGATTACTTAAGACTGTGTCAGTCAA 1364
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Analysis of the mouse transcriptome based on functional annotation 6 60,770 tull-length cDNAs
Nature 420, 561-573 (2002)
6 (bases 1 to 1689)
                                            785
                                                                                                                                                                            844
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tal: +82-42-860-4410
Fax: +82-42-860-4409
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Contact: Kim YS
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/organism="Homo sapiens"
/mol_type="mRNA"
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Padua-A.M., Gurske,W.A., Morin,D., Penn,S.G., Jovanovich,S.B.,
Plopper,C.G. and Buckpitt.A.R.
Gene expression analysis in response to lung toxicants: I.
Sequencing and microarray development
Am. J. Respir. Cell Mol. Biol. 30 (3), 296-310 (2004)
Contact: Shultz MA
Am. J. Respir. Cell Mol. Biol. 30 (3), 296-310 (2004)
Contact: Shultz MA
Am. Sholtz Mol. Biosciences, School of Veterinary Medicine
University of California, Davis
1311 Haring Hall, One Shields Avenue, Davis, CA 95616, USA
Tel: 530 752 4698
Email: mashultz@ucdavis.edu
Average Phred score is 20 or better. All poor quality data (Phred < 20) and vector/linker sequence has been removed.
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Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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/strain="Sprague-Dawley"
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/ Lissue_type="breast"
/ Lissue_type="breast"
/ Lissue_type="breast"
/ Lissue_type="blios"
/ Lissue_type="bl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Mashington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.B. Consortium/LiNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Lenghr. 217 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stops: 475.
Location/Qualifiers
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                                                                                                                                                                                                                                                                              AA631990 727 bp mRNA linear EST 28-OCT-1997 np74a05.81 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1132016 3' similar to SW:KCLK_MOUSE P22518 PROTEIN KINASE CLK ;, mRNA
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840 ATTGCCATTTTTAAAGGCCTTTACAGTGCCCTTTGTGTCCAGTGGTAAACGTGATTGGTC 899
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eucheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 727)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                   CTCAGCCTTGTGTTTTGAGCATAGGTGGCAT-CTTAATGAATATTACCTTGGTTTCA
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/organiem="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1132016"
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
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                                                                                                       548 TAGATTGGGATGAACACAGTTCTGCTGGTAGATATGTTAGGAGGCCCTGCAAACCGTTGA 489
                                                                                                                                                                                                            488 AGGAATITIAIGCITIIGICAIGAIGAAGAACAIGAGAACIGITIIGACCIGGITICGAAGAA 429
                                                                                                                                                                                                                                                                                              TTATITIGIACAGITAAGIGIAAAATATIGIATGITITIGIATCAATAGCATAATTAACTIG 189
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Scoring table:

Searched:

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Run on:

Minimum DB Maximum DB

Database

Result No.

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Sequence 1, Application US/09810671
Sequence 1, Application US/09810671
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Sequence 1, Application US/09810671
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GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
THEREOF INVENTION WIDMER:
CURRENT APPLICATION NUMBER:
CURRENT FILING DATE:
SOOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 2354
  4385, Ap
2299, Ap
3590, Ap
15332, A
1168, Ap
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14437, A
12776, A
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14390, A
14391, A
22, Appl
13504, A
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US-09-621-976-9631
US-09-313-294A-2299
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iive 0; Mismatches
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Best Local Similarity
Matches 2256; Conserv
     ; TYPE: DNA
; ORGANISM: Human
US-09-810-671-1
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(Ggn2_6/ptodata/1/ina/BCTUS_COMB.seq:*

(Ggn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

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                             GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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421 TITGGCAAAGTIGIAGAGTGCATTGATGCATGGCATGGCA	1201 GACCTGGTTCGAAGAATGTTAGAATGATCCAACTCAAGAATTACCTTGGATGAAGCA 1260 1272 GACCTGGTTCGAAGAATGTTAGAATTGATCCAACTCAAGAATTACCTTGGATGAGCA 1331 1261 TTGCAGCATCCTTTCTTGATTATTAAAAAGAAATGAAAT

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                                                                                  OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,000
FILING DATE: HEREWITH
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 2046.6;
Pred. No. 0;
0; Mismatches
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                                                                                                                                                                                                                                                                                                         NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90.7%;
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LENGTH: 2446 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOCY: linear
IMMEDIATE SOURCE:
                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                               FILING DATE: ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 95.8
Matches 2149; Conservative
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TELEX:
                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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CLONE: 339963
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                         AATTTTTCTTTTTGAAATTACCATTTTTAAATACCTTTGAAATATCCTTTGTGTCCAGTG
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AATTITITCITITIGAAATTACCATITITIAAATACCTITIGAAATATCCTITIGIGICCAGIG
                                                                                     ATGGAAAGGCATGCAGTTTGTCCATTGTGACAGTTTTGTTTAATAAAACCACATACACACT
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APPLICANT: Lal, Preeti
APPLICANT: Bandman, Olga
APPLICANT: Akerblom, Ingrid B.
APPLICANT: Shah, Purvi
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl G.
TITLE OF INVENTION: PROTBIN KINASE MOLECULES
CORRESPONDENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 9, Application US/09016000
; Patent No. 5962232
; GENERAL INFORMATION:
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CITY: Palo Alto
STATE: CA
COUNTRY: USA
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Db   1818 CTTGACTACTTTATACTTAAAGGATATTCTTTATATACTTCAAATTTAAACTTTAACACTTTATAAAGTTTTTCTTCTGTAATTGTTGAACGGGGGGTGATTATTATAACTCTGAATAACACACTTTAAAAGTTTTTCTCTGTAATTGTTGAACGGGGGGTGATTATTATAAACTCTGAAAAAACACAAAAAAATTTTTAAAAGTTTTTCTCTGTAAAAAAAA	RESULT 5 US-09-023-655-699 US-09-023-655-699 I GAPREAL INFORMATION: Patent No. 6607879 GENERAL INFORMATION: APPLICANT: Cocke G. Stuart APPLICANT: Susan G. Stuart APPLICANT: Susan G. Stuart TITLE OF INVENTION: TITLE OF INVENTION: EXPRESSION NUMBER OF SEQUENCES: 1508 COMPESSEE: INCYTE PHARMACEUTICALS, INC. STREET: 3174 PORTER DRIVE CITY: PALO ALTO STREET: CALIFORNIA CONDITES: CALIFORNIA CONDITES: BADDA G. COMPALIBLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/023,655 FILING DATE: RERENTH PRIOR APPLICATION DATA: PRIOR APPLICATION DATA: PRIOR APPLICATION DATA: FILING DATE: FILING D
	1214 GAATGTTAGAATATGATCCAAAGAATTACCTTGGATGAAGCATTGCAGCATCCTT 1273 1398 GAATGTTAGAATATGATCCAAACTAAAGAATTACCTTGGATGAAGCATTGCAGCATCCTT 1457 1274 TCTTTGACTTATTAAAAAGAAATGAAATGCAATCAGTGGTCTTACTATATATCTTCTT 1313 1458 TCTTTGACTTATTAAAAAGAAATGAAATGGGAATCAGTGGTCTTACTATATATCTTCTT 1517 1334 AGAAGAGATTACTTAAGAATGAAATGAACTAAACATCTAATATTTTTGTAAACATT 1577 1394 AAATTATTTTGTACAGTTAAGTGTAATTTTGTAACATTTTTTGTAACATT 1577 1358 AGAAGAGATTACTTAAGACTGTCAGTCAACATTTTTGTAAAATTAAC 1453 1518 AAATTATTTTGTACAGTTAAGTGTAAATTTGTATCAATAATTTTTGTAACATT 1577 1454 TTGTTAAGCAAGTAAGTGTAAATTTGTATGAATAATTAACTATTTTTTTT

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## PARCENT NO. 6/37513
## PARCENT NO. 6/37513
## PAPLICANT: ULLRICH, Axel
## APPLICANT: ULLRICH, Oliver
## APPLICANT: ULLRICH, Oliver
## TITLE OP INVENTION: CLK PROTEIN KINASES AND RELATED PRODUCTS AND METHODS
## TITLE OP INVENTION: CLK PROTEIN KINASES AND RELATED PRODUCTS AND METHODS
## CURRENT APPLICATION NUMBER: US/09/905,999
## CURRENT FILING DATE: 1999-07-31
## PRIOR PILING DATE: 1999-07-31
## PRIOR PILING DATE: 1997-06-17
## PRIOR PILING DATE: 1996-12-19
## NUMBER: OF SEQ ID NOS: 26
## SEQ ID NO 26
## LENGTH: 1549
                                                                                                                              CTCAGAAAAIGITIACTGTIAGAATTCTATTAAATTTTAAAGTGTIGTATTCTTTTCATT 1830
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                                                                                                                                                                                                                                              CAGTITIGITITAATAAAACCACATACACACTITIAAGATTAAAATCTAACTGGAAAGT
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Pred. No. 1.1e-277;
0; Mismatches 121; Indels 0;
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ilarity 90.6%;
Conservative
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US-09-905-999-26
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Best Local Simi
Matches 1170;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1178.2; DB 4; Length 1456;
Pred. No. 6.7e-299;
0; Mismatches 3; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTTGGAGCATAGGTTGCATTCTTATTGAATATTAC
                                    NAME: Zeller, Karen J.
REGISTATION WUMBER: 37,011
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
FELERAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 699:
SEQUENCE CHARACTERISTICS:
LENGTH: 1456 base pairs
TYPE: nucleic acid
STRANDENESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                      52.2%;
                  ATTORNEY/AGENT INFORMATION: NAME: Zeller, Karen J.
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 99.74
Matches 1191, Conservative
                                                                                                                                                                                                                                                                                                                          ; LIBRARY: HNT2AGT01
; CLONE: 488842
US-09-023-655-699
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OY 1274 TCTTTGACTTATTAAAAAGAAATGAAATGG 1304 	RESULT 7 US-09-810-671-3  US-09-810-671-3  Sequence 3, Application US/09810671  Patent No. 63-55291  GENERAL INFORMATION:  TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  TITLE OF INVENTION: THEREOF  TILLE OF INVENTION: THEREOF  TILLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  TILLE OF INVENTION: ACID MOLECULES OF SECULES OF SECULE	NOMES OF SECTION OF SEC	Query Match 48.6%; Score 1097; DB 3; Length 21234; Best Local Similarity 100.0%; Pred. No. 5.4e-277; Matches 1097; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	OY 1157 AGGAATTTATGCTTTGTCATGATGAAGAACATGAGAAACTGTTTGACCTGGTTCGAAGAA 1216  DD 18138 AGGAATTTATGCTTTGTCATGATGAAGAACATGAGAAACTGTTTGACCTGGTTCGAAGAA 18197	OY 1217 TGTTAGAATATGATCCAACTCAAAGAATTACCTTGGATGAAGCAFTGCAGCATCCTTTCT 1276	OY 1277 TTGACTTAITAAAAAGAAATGAAATGAGAATCAGTGGTCTTACTATATACTTCTCTAGA 1336  Db 18258 TTGACTTAITAAAAAGAAATGAGAATCAGTGGTCTTACTATATATACTTCTTGAGA 18317	Oy 1337 AGAGATTACTTAAGACTGTGAGGACACTAAACATTCTAATATTTTGTAAACATTAAA 1396 	OY 1397 TTAITITGTACAGITAAGIGTAAATATIGTATGTTTGTATCAATAGCATAATTAACTIG 1456  Db 18378 TTAITITGTACAGITAAGIGTAAATATIGTATGTTTTGTATCAATAGCATAATTAACTIG 18437	Qy 1457 TTAAGCAAGTATGGTCTTGATAATGCATTAGAAAATTAAATTTTCTTTTTGAA 1516	Qy 1517 ATTACCATTTTAAATACCTTTGAAATATCCTTTGTGTCCAGTGATAAATGTGATTGAT	OY 1577 TIGCCTITIGRACATGGAGGTCACCTCTGAAGTGATTTTTTTGAGTAAAAGGAAATCTT 1636  Db 18558 TIGCCTTTTGTACATGGAGGTCACCTCTGAAGTCATTTTTTTT	OY 1637 GACTACTTATATTCTTAAAGGAATATTCTTATATACTTCAAATTTAGAACTTAACTTT 1696  Db 18618 GACTACTTTATATTCTTAAAGGAATATTCTTTATATACTTCAAATTTAGAACTTAACTTT 18677		OY 1757 ACTAGAAACTAGAAAATGTTTACTGTTAGAATTCTATTAAATTTTAAGTGTG 1816 
194 AAAGGAAGGGAATAGACACTGTTCAAGTCATCAGTCACGTTCGAAGACCACCGAAGGA 253 		434 INCOCCATACCEGAGGGGTCTTCTGGAATCCAAGTATTGGGGGCTTGAACGGG 718 659 TAGGACGTTACCGGGAGGCAGCTCGTTCTGAATCCAAGTATTGGAGGACTTGAACAGCA 718 494 CTGATCCCAATAGTGTCTTCCGATGTGTCCAAGAGTGCTAGAACAGTATTGATCATCATGGTC 553  111	554 AIGTITGTATTGTGTTTGAACTACTGGGACTTAGGACTTTCGTTAAAGAAAACA 613 	614 GCTTTCTGCCATTTCAAATTGACCACATCAGGCAGATGGCGTATCAGATCTGCCAGTCAA 673 	674 TAAATITTTTACATCATAATAAATTAACCCATACAGATCTGAAGCCTGAAAATATTTGT 733 	734 TIGIGAAGTCIGACTAIGTAGTCAAATATAATICTAAAATGAAACGTGATGAACGCACAC 793 	794 TGAAAAACACAGATATCAAAGTTGTTGACTTTGGAAGTGCAACGTATGATGATGATGATGACTC 853 	854 ACAGTACTTTGGTGTCTACCGGGCTCTACAGAGCTCCCGAGGTCATTTTGGCTTTAGGTT 913 	914 GGTCTCAGCCTTGTGATGTTTGCAGCATAGGTTGCATTCTTATTGAATATTACCTTGGTT 973 	974 TCACAGTCTTTCAGACTCATGATAGTAAAGAGCACCTGGCAATGATGGAACGAATATTAG 1033 	1034 GACCCATACCACACACATGATTCAGAAAACAGAAAAGGCAAGTATTTTCACCATAACC 1093 	1094 AGCTAGATTGGGATGAACACAGTTCTGCTGGTAGATATGTTAGGAGACGCTGCAAACCGT 1153 	1154 TGAAGGAATTTATGCTTTGTCATGAAGAACATGAGAAACTGTTTGACCTGGTTCGAA 1213 	1214 GAATGTTAGAATATGATCCAACTCAAAGAATTACCTTGGATGAAGGATTGCAGCATCCTT 1273 

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Qy 1337 AGAGATTACTTAAGACTGTGTCAGTCAACTAAACATTCTAATATTTTTGTAAACATTAAA 1396	Qy 1397 TTATTTTGTACAGTTAAGTGTAAATATTGTATGTTTTGTATCAATAGCATAATTAACTTG 1456  Db 18378 TTATTTGTACAGTTAAGTGTAAATATTGTATGTTTTGTATCAATAGCATAATTAACTTG 18437	OY 1457 TTAAGCAAGTATGGTCTTGATAATGCATTAGAAAATTAAAATTAATT	Qy 1517 ATTACCATTTTAAATACCTTTGAAATATCCTTTGTGTCCAGTGATAAATGTGATTGAT	Qy 1577 TTGCCTTTTGTACATGGAGGTCACCTCTGAAGTGATTTTTTTT	Qy 1637 GACTACTTTATATTCTTAAAGGAATATTCTTATATACTTCAAATTTAGAACTTAAACTTT 1696	Qy 1697 AAAAGTTTTTCTTCTGTAATTGTTGAACGGGTGATTATTATTAACTCTAGATAAGGGT 1756	Oy 1757 ACTAGAAACCCAGAAATGTTTACTGTTAGAATTCTATTAAATTTTAAGTGTTG 1816	Qy 1817 TATTCTTTTCATTGGGTGATGTCAGGGTGATACCAGACATTCATGGAAAGGCATGCAG 1876	Qy 1877 TITGTCCATRGIGACAGITTGTTAATAAAACCACATACACACTTTATTTAAGATTAAAA 1936	OY 1937 TCTAACTGGAAAGTCAGCTTGGAAAATGGACATTTCCAAGTATGTTTGGTGAGTCACAGA 19	QY 1997 TATAAAATAGAAATTCTGATGAGAGGTTTCAGTTTTAATACCAAGTCCTTAGGAGTCT 20	OY 2057 TAACATTGGCCAGCATCTGTTTATCAAATGACATAAATACGTAAACCTATAAGATTAAG 2116	OY 2117 TITATTAATTAGGCAATTTATGTCTGGGAAATTACGGGAGAAAGAGGATTTGATTG 2176	Oy 2177 GAAAGCAGTTTGGGAAGAAGTGCTGCTGAAATTTCCAGAATTTAATTGATTG	Qy 2237 AAACTTTTGACTTCAG 2253 	RESULT 9 US-10-339-656-3 ; Sequence 3, Application US/10339656 ; Patent No. 6733978 ; GENERAL INPORMATION;	; APPLICANT: YAN, Chunhua et al. ; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
1817 TATTCTTTTCATTGGGTGATGTCAGGGTGATAACCAGACATTCATGGAAAGGCATGCAG 1876 	1877 TTTGTCCATTGTGACAGTTTGTTTAATAAAACCACATACACACTTTATTAAGATTAAAA 1936 	1937 TCTAACTGGAAAGTCAGCTTGGAAAATGGACATTTCCAAGTATGTTTGGTGAGTCACAGA 1996 	1997 TATAAAATTAGAAATTCTGATGAGGGTTTCAGTTTTTAATACCAAGTCCTTAGGAGTCT 2056 	2057 TAACATTGGCCAGCATCTGTTTATCAAATGACATAAATACGTAAACCTATAAGAATTAAG 2116 	2117 TTTATTAATTAGGCAATTTATGTCTGTGATAATTCTTAGGGAGAAAGGGATTTGATTG 2176 	2177 GAAAGCAGTTTGGGAAAGTGCTGGTGAATTTCCAGAATTTAATTGATTG	2237 AAACTTTTGACTTCAG 2253 	SULT 8 -10-109-854-3	equence s, Application US/IO109834 atent No. 6630337 ENERAL INFORMATION: APPLICANT: YAN, Chumhua et al.	TILLE OF INVENTION: LOCATED HUMAN ALMASE FROIEIRS, NUCLEIC TITLE OF INVENTION: THEREOF TITLE OF INVENTION: THEREOF FILE REFERENCE: CLOOO758DIV	CORRENT AFFILIATION NUMBER: 05/10/109,854 CURRENT FILING DATE: 2002-04-01 PRIOR APPLICATION NUMBER: 60/227,470 PRIOR FILING DATE: 2000-08-24	FRIOR FILING DATE: 2001-03-19 NUMBER OF SEQ ID NOS: 5 SOFTWARE: PastSEQ for Windows Version 4.0	SEQ 1D NO 3 TENGTH: 21234 TYPE: DNA ORGANISM: Homio sapien	48.6%; Score 1097; DB 4; Length 21234; milarity 100.0%; Pred. No. 5.4e-277;	rational de la comparacte de la comparac	1217 IGITAGAATATGAICCAACTCAAAGAATTACCTTGGATGAAGCATTGCAGCATCCTTTCT 1276	TTGACTTATTAAAAAAGAAATGAAATGGGAATCAGTGGTCTTACTATATACTTCTCTGGA

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18978 TATAAAATAGAAATTCTGATGAGGTTTCAGTTTTTTAATACCAAGTCCTTAGGAGTCT 19037
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APPLICANT: Kaser, Matthew R.
APPLICANT: Kaser, Matthew R.
TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES FILE REPERBYCE: PA-0035 US
CURRENT APPLICATION NUMBER: US/09/919,039
CURRENT FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: 60/222,113
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 401
SOFTWARR: PERL PROGRAM
SEQ ID NO 238
LENGTH: 2254
                                                                                                                                                                                                                                                                                                                                        1163 TACTITCCGCTGTGTCCAGATGTTGGAATGGTTTGAGCATCATGGTCACATTTGCATTGT
                      1937 TCTAACTGGAAAGTCAGCTTGGAAAATGGACATTTCCAAGTATGTTTGGTGAGTCACAGA
                                                                                                                                                                             TAACATTGGCCAGCATCTGTTTATCAAATGACATAAATACGTAAACCTATAAGAATTAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6727066 420527.25
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LOCATION: 231, 241
COTHER INFORMATION: a, t, c, g, or other
US-09-919-039-238
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Patent No. 6727066
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US-09-919-039-238
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TITLE OF INVENTION: THEREOF

CURRENT APPLICATION NUMBER: US/10/339,656

CURRENT FILING DATE: 2003-01-10

PRIOR APPLICATION NUMBER: 10/109,854

PRIOR FILING DATE: 2002-04-01

PRIOR FILING DATE: 2001-03-19

PRIOR FILING DATE: 2000-08-24

NUMBER OF SEQ ID NOS: 5

SOFTWARE: PASESEQ for Windows Version 4.0

SERVETH: 21234
                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapien
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GENERAL INFORMATION:

APPLICANT: ULISICH, Axel

APPLICANT: ULISICH, Axel

APPLICANT: ULISICH, Oliver

TITLE OF INVENTION: CLK PROTEIN KINASES AND RELATED PRODUCTS AND METHODS

FILE REFERENCE: 038602/0431

CURRENT APPLICATION UNMER: 05/127,248

PRIOR APPLICATION NUMBER: 05/127,248

PRIOR PILING DATE: 1999-07-31

PRIOR PILING DATE: 1999-06-17

PRIOR PELING DATE: 1999-06-17

PRIOR APPLICATION NUMBER: US 60/034,286

PRIOR FILING DATE: 1997-06-17

PRIOR PILING DATE: 1995-12-19

NUMBER OF SEQ ID NOS: 26

SEQ ID NOS: 26

SEQ ID NO 22

TENGRAL 1512
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Pred. No. 5.5e-116;
0; Mismatches 398; Indels
                                                                                                                                                                                                                                                                                                                                                                      Query Match
21.3%;
Best Local Similarity 64.6%;
Matches 736; Conservative
                                                                                                                                                                                                                                                                                                         TYPE: DNA
CORGANISM: Mus musculus
US-09-905-999-22
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                                                                                               1283 TCGACTGGATCATATCAGAAAGATGGCATATCAGATATGCAAGTCTGGAATTTTTTGCA
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                                                                   TCANATTGACCACATCAGGCAGATGGCGTATCAGATCTGCCAGTCAATAAATTTTTTACA
                                                                                                                             TCATAATAAATTAAACCCATACAGATCTGAAGCCTGAAAATATTTTGTTGAAGTCTGA
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. Sequence 22, Application US/09905999; Patent No. 6797513

RESULT 11 US-09-905-999-22

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CCTTGGTTTCACAGTCTTTCAGACTCATGATAGTAAAGAGCACCTGGCAATGATGGAACG 1025
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                                    126 AAAAAATGTAGGCCGTTACCGTGAAGCAGCTCGTTCAGAAATCCAAGTATTAGAGCACTT
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Patent No. 6500938
GENERAL INPORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Sellhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
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| Sequence 24, Application US/09905999|
| Sequence 24, Application US/09905999|
| Sequence 24, Application US/0905999|
| SERVERAL INFORMATION:
| APPLICANT: ULLRICH, Axel |
| APPLICANT: NAYLER, Oliver |
| TITLE OF INVENTION: CLK PROTEIN KINASES AND RELATED PRODUCTS AND METHODS |
| TITLE OF INVENTION: CLK PROTEIN KINASES AND RELATED PRODUCTS AND METHODS |
| FILE REFERENCE: 038602/0431 |
| CURRENT APPLICATION NUMBER: US/09/905,999 |
| CURRENT FILING DATE: 1999-06-17 |
| PRIOR PILING DATE: 1990-06-17 |
| PRIOR PILING DATE: 1990-12-19 |
| COMMUNICATION NUMBER: US 60/034,286 |
| COMMUNICATION NUMBER: US 60/034,286 |
| COMMUNICATION NUMBER: US 60/034,286 |
| PRIOR PILING DATE: US 60/034,286 |
| COMMUNICATION NUMBER: US 60/034,286 |
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Pred. No. 5.1e-109;
0; Mismatches 362;
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US-09-905-999-24
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Matches 672;
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US-09-905-999-24
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Sequence 2648, Application US/09949016

Sequence 2648, Application US/09949016

Batent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REPERRENCE: CLOO1307

CURRENT APPLICATION NUMBER: 00/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH- 1529
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    726 TATTTTGTTTGTAAGTCTGACTATGTAGTCAAATATAAATTGAAACGTGATGA
                                              920 CATCCTGTTTGTGAATTCTGAGTTTGAAACCCTCTACAATGAGCACAAAAGGGCTGTGAGGA
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Best Local Similarity 63.5
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ORGANISM: Human
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                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
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Pred. No. 3.8e-103;
0; Mismatches 376;
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1439:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19.2%;
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Best Local Similarity 63.6
Matches 658; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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US-09-016-434-1439
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Query Match
Best Local Similarity 63.5%;
Matches 657; Conservative (
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; ORGANISM: Human
US-09-949-016-2649
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                 620 ccgcaacigegecaagiacegeaegeciecegeciaeaaaircaacerecieaaaaar
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US-09-949-016-2649
; Sequence 2649, Application US/09949016
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GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
FRIOR PELING DATE: 2000-10-20
FRIOR PELING DATE: 2000-10-03
FRIOR FILING DATE: 2000-09-08
NUMBER: 60/231,498
FRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FRAESEQ FOR WINDOWS VERSION 4.0
SEQ ID NO 2649
LEGISLATH: 1763
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Pred. No. 1e-102;
0; Mismatches 377; Indels
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1086 CCATAACCAGCTAGATTGGAACGACACAGTTCTGCTGGTAGATATGTTAGGAGACGCTG 1145
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Job time : 382.816 secs
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	Description	Aad32038 Human kin	Aaf89402 Human cel	Aaf44675 Novel pro	Adi29373 Human MAR	Aax89852 Human pro	Adp24393 PRO polyp	Adi26142 Human cDN	Aac81772 Human bea	Ado07809 Human pol	Adi26140 Human cDN	Aac59283 Human sec	Adi31373 Human cDN	Adi26144 Human cDN	Ado07812 Mouse pol	Aad32039 Human kin	Ado07810 Human pol	Adh58708 Human CDC	Adr14000 Human NF-	Adp24718 PRO polyp	Ado07813 Mouse pol
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assays, identifying modulators of kinase activity or treating disorders characterized by absence or unwanted expression of the protein.

Claim 4; Fig 1; 81pp; English

The invention relates to isolated human kinase proteins and nucleic acids. The nucleic acid and peptide sequences can be used as models for the development of human therapeutic targets, aid in the identification of therapeutic proteins and serve as targets for the development of human therapeutic agents that modulate kinase activity in cells and tissues that express the kinase. The nucleic acids are useful as probes or primers, in constructing recombinant vectors, for expressing antigenic portions of the proteins, chromosome mapping, drug screening, testing an individual for a genotype, and for gene therapy in patients containing cells that are aberrant in kinase gene expression. The proteins may be used in drug screening assays, in the identification of compounds that canalysis, in treating disorders characterised by an absence or unwanted expression of the protein (bone osteosarcoma, or colon-moderately expression of the protein (bone osteosarcoma, or colon-moderately in vitro, or in cell lysate or supernatant, to isolate and purify the in vitro, or in cell lysate or supernatant, to isolate and purify the protein function. The present squence is human protein cDNA. Human kinase protein gene is located on chromosome 5 

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                                                                                                                                                                                                                                                                                                                                                      GTCATTATTTAGAAGCAAGGTCCTTGAATGAGCGAGATTATCGGGACCGGAGATACGTTG
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                                                                                      TAAATITITAAGTGTTGTATTCTTTTTCATTGGGTGATGTCAGGGTGATAACCAGACATTC
                                                                                                                                                                                          TTATTTAAGATTAAAATCTAACTGGAAAGTCAGCTTGGAAAATGGACATTTCCAAGTATG
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                                      CTCTAGATAAGCAGGTACTAGAAACCAAAACTCAGAAAATGTTTACTGTTAGAATTCTAT
                                                                           TAAATITITAAGTGTTGTATTCTTTTTCATTGGGTGATGTCAGGGTGATAACCAGACATTC
                                                                                                                           AFGGAAAGGCATGCAGTTTGTCCATTGTGACAGTTTGTTTAATAAAACCACATACACACT
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                                                                                                                                                                                                                             TITGGTGAGTCACAGATATAAAAATAGAAATTCTGATGAGAGGTTTTCAGTTTTTAATACC
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TITAGAACTIAACTITAAAAGTITITCTTCTGTAATTGTTGAACGGGTGATTATTAA
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                         CTCTAGATAAGCAGGTACTAGAAACCAAAACTCAGAAAATGTTTACTGTTAGAATTCTAT
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P-PSDB; AAB69705.
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Db 2191 AAATCTAACTGGAAATTGGAAAATGGACATTTCCAAGTATGTTTGGTCAGTCA	RESULT: 3 APR44675 standard; CDNA; 2488 BP.  APR44675 DY APR44675 DY APR44675 DY APR44675 DY APR44675; DY APR44675; DY APR44675; DY APR44675; DY APR44675; DY APR44675; AND BY BY AND BY BY AND BY BY AND BY AND BY BY BY AND BY	
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activity include rheumatoid arthritis, atherosclerosis, autoimmune disorders, complications of organ transplantation, myocardial infarction, immune disorders, cardiomyopathies, strokes, renal failure, oxidative-stress related disorders, chronic inflammatory bowel disease, chronic inflammatory bowel disease, chronic inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis, psoriasis, rhinitis, autoimmunity, diabetes, cancers and reproductive disorders
                                                                                     Query Match
Best Local Similarity 95
Matches 2148; Conservativ
                                                                                                                                                     854 ACAGTACTTTGGTG
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1088 ACAGTACTTTGGTG
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0; Mismatches         1; Indels         90; Gaps           GCTCTTGAATGAGCGAGATATCGGGACCGGAGATACGTTG	47 CO	115
	Qy 1154 TGAAGGAATTTATGCTTTGTCATGAAGAACATGAGAAACTGTTTGACCTGGTTCGAA 	GAA 1213     GAA 1447
	Qy 1214 GAAIGTIAGAATAIGAICCAACTCAAGAATTACCTIGGAIGAAGCAITGCAGCAICCTT	CTT 1273     CTT 1507
	Qy 1274 TCTTTGACTTATTAAAAAGAAATGAAATGGGAATCAGTGGTCTTACTATATACTTCTCT	rcr 1333      CT 1567
	Qy 1334 AGAAGAGTTACTTAAGACTGTGTCAGTCAAACATTCTAATATTTTTGTAAACATT 	ATT 1393     ATT 1627
SATATGAAATCGTGGACACTTTGGGTGAAGGAGCCTTTGGCAAAGTTG 373	Qy 1394 AAATTATTTTGTACAGTTAAAGTGTAAATATTGTATGTTTTGTATCAATAGCATAATTAAC 	AAC 1453     AAC 1687
	Qy 1454 TTGTTAAGCAAGTATGGTCTTGATAATGCATTAGAAAATTAAAATTAAAATTTTTTTT	TTT 1513      TTT 1747
	Qy 1514 GAAATTACCATTTTAAATACCTTTGAAATATCCTTTGTGTCCAGTGATAAATGTGATTG	TTG 1573     TTG 1807
	Qy 1574 ATCTTGCTTTTGTACATGGAGGTCACCTCTGAAGTGATTTTTTTT	AAT 1633     AAT 1867
	Qy 1634 CTTGACTACTTTATATTCTTAAAGGAATATTCTTTATATACTTCAAATTTAGAACTTAAC 	AAC 1693     AAC 1927
	Qy 1694 TTTAAAAGTTTTCTTCTGTAATTGTTGAACGGGTGATTATTAACTCTAGATAAGCA 	GCA 1753         
Eg ca	Qy 1754 GGTACTAGAAACCCAAAATGTTTACTGTTAGAATTCTATTAAATTTTAAGTG Db 1988 GGTACTAGAAACCAAAACTCAGAAAATGTTTACTGTTAGAATTCTATTAAATTTTAAGTG	STG 1813     STG 2047
GAC TGT	QY 1814 TTGTATTCTTTTCATTGGGTGATGTCAGGGTGATAACCAGACATTCATGGAAAGGCATG  DD 2048 TTGTATTCTTTTCATTGGGTGATGTCAGGGTGATAACCAGACATTCATGGAAAGGCATG	ATG 1873     ATG 2107
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                                                            2347
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                                                                                            2348 AAGTITATIAATIAAGGCAATITATGTCTGTGAIAATITCTTACGGGAGAAAGAGGATITGA 2407
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             AGATATAAAAATATGATGATGAGAGGTTTCAGTTTTTAATACCAAGTCCTTAGGAG
                                                    TIGGAAAGCAGITIIGGGAAGAAGIGCIGCIGAAAITIICCAGAAITIIAAITGAIIGGITA
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                                                                                 AAGTTTATTAATTAGGCAATTTATGTCTGTGATAATTCTTACGGGAGAAAGAGGATTTGA
                                                                                                                                                                                                                                                                                                                              Human; ss; antisense gene therapy; MARK3;
MAP/microtubule affinity-regulating kinase 3; cancer;
Alzheimer's disease; neurodegenerative disorde;
hyperproliferative disorder; cytostatic.
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                                                                                                                                        14 GTCATTATTTAGAAGCAAGGTCCTTGAATGAGCGAGATTATCGGGACCGGAGATACGTTG
                                                                  Gaps
                                                                  90;
                                 Length 2488;
Seguence 2488 BP; 819 A; 400 C; 504 G; 764 T; 0 U; 1 Other;
                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                    518 AAAGGAAGCGCAATAGACACTGTTCAAGTCATCAGTCACGTTCG-
                                  DB 12;
                                                                    1;
                                                                    0; Mismatches
                               Score 2048;
Pred. No. 0;
                                  90.8%;
                                                       Best Local Similarity 95.5
Matches 2148; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention provides human protein kinase molecules (HPKM) (AAY27052-57) and nucleic acid sequences (AAX89850-55) encoding the HPKM polypeptides can be produced recombinantly by standard recombinant methodology. Protein kinases add phosphate groups to proteins. HPKM polypeptide or an HPKM antagonist is used to treat or prevent cancer or an immune disorder. The present sequence represents the nucleotide sequence of HPKM-3
                               2348 AAGITITATITAATITAGGCAATITATGTCTGTGATAATTCTTACGGGAGAAGAAGGATTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  288 GTCATTATTAGAAGCAAGGTCCTTGAATGAGCGAGATTATCGGGACCGGAGATACGTTG
               AAGTTTATTAATTAGGCAATTTATGTCTGTGATAATTCTTACGGGAGAAAGAGATTTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90;
                                                                                                                                                                                                                                                                                                                                     Human protein kinase (HPKM)-3 encoding nucleotide (clone ID
                                                                                                                                                                                                                                                                                                                                                                Human protein kinase molecule; HPKM; human; protein kinase;
phosphate group; cancer; immune disorder; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2446 BP; 788 A; 391 C; 516 G; 751 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 8; Page 74-75; 77pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            128. .1483
/*tag= a
/product= "HPKM-3"
                                                                                                                                  CATAAACTTTTTGACTTCA 2252
                                                                                                                                                                                                                                            BP.
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                                                                                                                                                                                                                                                                                                       (first entry)
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Guegler KJ;
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Matches 2149;
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                                         1268 GACCCATACCACACACATGATTCAGAAAACAAGAAAACGGAAGTATTTTCACCATAACC
                                                                                                       1328 AGCTAGATTGGGATGAACACAGTTCTGCTGGTAGATATGTTAGGAGACGCTGCAAACCGT
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TCACAGTCTTTCAGACTCATGATAGTAAAGAGCACCTGGCAATGATGGAACGAATATTAG
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                          GACCCATACCACAACACATGATTCAGAAAACAAGAAAACGCAAGTATTTTCACCATAACC
                                                                                       AGCTAGATTGGGATGAACACAGTTCTGCTGGTAGATATGTTAGGAGACGCTGCAAACCGT
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	494 CTGATCCCAATAGTGTCTTCCGATGTGTCCAGATGCTAGAATGGTTTGATCATCGTCG 553  [	### ##################################

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2418 CATAAACTTTTGACTTCAAAAA 2440
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ADP24393 standard; cDNA; 1814 BP 18-NOV-2004 (first entry) Unidentified. ADP24393; RESULT 6
ADP24393
ADP

PRO polypeptide encoding cDNA SEQ ID NO:1571.

ss; gene; PRO; antinflammatory; antiarthritic; antirheumatic; immunosuppressive; osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic; antiasthmatic; hepatotropic; respiratory; gene therapy; immune system.

WO2004041170-A2.

21-MAY-2004.

30-OCT-2003; 2003WO-US034312.

01-NOV-2002; 2002US-0423394P

(GETH ) GENENTECH INC

Van Lookeren M, Williams PM, Wood WI; Schoenfeld J, Clark H, W ID;

WPI; 2004-419628/39. P-PSDB; ADP24394 New PRO polypeptides and polynuclectides, useful for treating e.g. erythematosus, rheumatoid arthritis, diabetes mellitus, immune-mediated renal disease, or demyelinating diseases of the central or peripheral nervous system.

Claim 1; SEQ ID NO 1571; 2940pp; English

idiopathic inflammatory myopathy. Siggren's syndrome, systemic curetors, an idiopathic inflammatory myopathy. Siggren's syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopatha, thyroiditis, diabetes mellitus, immune-mediated renal disease, a demyelinating disease of the central or peripheral nervous system, idiopathic demyelinating polymeuropathy, dullain-Barre syndrome, a chronic inflammatory demyelinating polymeuropathy, a hepathis, primary infectious or autoimmune chronic active hepathis, primary biliary cirrhosis, granulomatous hepathis, solerosing cholangitis, inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's disease, an autoimmune or immune-mediated skin disease, a bullous skin disease, asthma, allergic rhinitis, atopic dermathis, food hypersensitivity, urticaria, an immunologic disease of the lung; cosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity pneumonia, idiopathic pulmonary consulpathic pneumonia, idiopathic pulmonary consulpathic pneumonia, idiopathic pulmonary consulpathic pneumonia, idiopathic pneumonia, graft rejection or graft-versus-host disease. The present sequence encodes a PRO protein of The invention relates to a novel isolated nucleic acid and the PRO polypeptide encoded by it. A protein of the invention has antiinflammatory, antiarthritic, antiinheumatic, immunosuppressive, osteopathic, antidiabetic, dermatological, antipsoriatic, antidialergic, antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide of the invention may have a use in gene therapy. The PRO polypeptide, its agonist, or antibody that specifically binds to the polypeptide is useful for treating an immune related disorder such as systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile, chronic arthritis, a spondyloarthropathy, systemic sclerosis, an

Sequence 1814 BP; 609 A; 299 C; 385 G; 520 T; 0 U; 1 Other;

Query   Best L	ery Match 72.3%; Score 1632; Local Elmilarity 99.3%; Pred. No. 0; Prhes 1638. Concertative 0. Mismatches	DB 1
ò	14 GT	cerre 73
DP	161 GTCATTATTTAGAAGGACGGTCCTTGAATGAGCGAGATTATCGGGACCGGAGATA	CGTT
ò	7	CATTG 13
qq	-	28
ර ස	134 AAAGCGGTATCGAATCCACTGCAGTAAATCTTCAGTCCGCAGCAGGAGAAGCAGTCCTA	
3 8	94	ני ני
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ò	254 AAAGATCCAGGAGTATAGAGGATGATGAGGGGGCTCACCTGATCTGTCAAAGTGGAGACG	GGTCACCTGATCTGTCAAGTGGAGACG 313
Db	401 AAAGATCCAGGAGTATAGAGGATGATGAGGGA	GGTCACCTGATCTGTCAAAGTGGAGACG 460
ò	314 ITCTAAGAGCAAGATATGAAATCGTGGACACTTTGGGTGAAGGAGCCTTTGGCAAAGTTG	TTGGGTGAAGGAGCCTTTGGCAAAGTTG 373
QQ	461 TICTAAGAGCAAGATATGAAATCGTGGACAC	tiggergaaggactiitgecaaagirg 520
ò	374 TAGAGTGCATTGATCATGGCATGGATGCATGCATGTAGCAGTGAAAATCGTAAAAATG	43
ପ୍ର	521 radagrecarrearcarescarescare	cargradadadadadadadada 580
ò	434 TAGGCCGTTACCGTGAAGCAGCTCGTTCAGAA	CAGCTCGTTCAGAAATCCAAGTATTAGAGCACTTAAATAGTA 493
qq	581 TAGGCCGTTACCGTGAAGCAGCTCGTTCAGA	ATCCAAGTATTAGAGCACTTAAATAGTA 640
٥y	494 CIGATCCCAATAGTGTCTTCCGATGTGCCAGATGCTAGAATGGTTTGATCAT	ATGCTAGAATGGTTTGATCATCATGGTC 553
Op	641 CIGAICCCAAIAGIGICTICCGAIGIGICCAC	AIGCIAGAAIGGIIIGAICAICAIGGIC 700
λŏ	554 AIGITIGIAITIGAACIACIGGGACITAGIACITACGAITICAITAAAGAAAACA	AGTACTTACGATTTCATTAAAGAAAACA 613
Dp	701 AIGHTHGHATTGTGTTTGAACTACTGGGACTI	AGTACTTACGATTTCATTAAAGAAAACA 760
ò	614 GCTTTCTGCCATTTCAAATTGACCACATCAGGCAGATGGCGTAT	CAGATGGCGTATCAGATCTGCCAGTCAA 673
qq	761 GCTTTCTGCCATTTCAAATTGACCACATCAGG	
à	674 TAAATTTTTTACATCATAATAAATTAACCCATACAGATCTGAAGCCTGAAAATATTTTGT	ACAGATCTGAAGCCTGAAAATATTTTGT 733
qq	821 TAAATTTTTTACATCATAATAAATTAACCCA	ACAGATCTGAAGCCTGAAATATTTTGT 880
à	734 TTGTGAAGTCTGACTATGTAGTCAAATATAA3	CTGACTATGTAGTCAAATATATATTCTAAAATGAAACGTGATGAACGCACAC 793
QQ	881 TTGTGAGTCTGACTATGTAGTCAAATATAA	-8 -8
ŏ	794 IGABAAACACAGATATCAAAGTTGTTGACTTTGGAAGTGCAACGTATGATGATGAACATC	GGGAAGTGCAACGTATGATGATGAACATC 853
Dp	941 TGAAAACACAGATATCAAAGTTGTTGACTTT	GGAAGTGCAACGTATGATGAACATC 1000
δλ	854 ACAGTACTTTGGTGTCTACCCGGCACTACAG	CACTACAGAGCTCCCGAGGTCATTTTGGCTTTTAGGTT 913
QQ	-8 -8	gerecedadareartingerriadarr 1060
ò	914 GGTCTCAGCCTTGTGATGTTTGGAGCATAGGT	CTTGTGATGTTTGGAGGATGCATTCTTATTGAATATTACCTTGGTT 973
Ωp	TCAGC	rgcárrcrtárrgaárarraccrrggrr 1120
ģ	974 TCACAGTCTTTCAGACTCATGATAGTAAAGAGCACCTGGCAATGATGGAACGAAC	CACCTGGCAATGATGGAACGAATATTAG 1033
d d	1121 icacagiciticagacicaigatagaagad	cacciegeaaigaiggaacgaaiaiiag 1180
ò	1034 GACCCATACCACACACATGATTCAGAAAAC	CATACCACAACACATGATTCAGAAAACAAGAAAACGCAAGTATTTTCACCATAACC 1093

FATTAGE 2

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The invention relates to a purified protein promoting signal transducer and activator of transcription 6 activation (STAT6). The protein is useful for the producing an antibody, which involves administering the protein or its epitope-bearing fragments to a non-human animal as an antigen. The nucleic acid is useful for diagnosing a disease or susceptibility to a disease related to expression or activity of the protein. A transformant expressing the protein is useful for screening compounds which inhibit or promote STAT6 activation. A transformant expressing the protein is useful for producing a pharmaceutical composition. Compositions, antibodies and antisense molecules are useful for the treating a disease associated with STAT6 activation such as allergic diseases, inflection, autoimmune diseases, diabetes, hyperalpidaemia, infections disease and cancers. Compositions are useful for treating disease associated with STAT6 activation and/or prevention for treating diseases. Compositions are also useful in rheumatoid arthritis, osteoarthritis, systemic lupus erythematosus, sepsis, asthma, allergic rhinitis, ischaemic heart diseases, subarachnoid haemorrhage, viral hepatitis and AIDS. The protein has efficient promoting STAT6 compounds for treating and preventing disease associated with excessive compounds for treating and prevent alseases associated with excessive compounds for treating and prevent assessed expresents a persent sequence represents a persent events.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          161 GTCATTATTTAGAAGCAAGGTCCTTGAATGAGCGAGATTATCGGGACCGGAGATACGTTG
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                                                                                                                                                                         New signal transducer and activator of transcription 6 activation promoting purified protein, for diagnosing and treating disease associated with activation/inhibition of transcription factor e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 12; Length 1792;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 activation or inhibition of STAT6. The present sequence repret
human cDNA encoding a protein which promotes STAT6 activation
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                                                                                       Ishizawa
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                                                                                       Muramatsu S,
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                                                                                                                                                                                                                                                                    claim 4; SEQ ID NO 107; 1368pp; English
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                                                                                         Honda
15-MAY-2003; 2003JP-00137505.
16-MAY-2003; 2003US-0470836P.
                                                                                       Sugahara T, Matsuda A,
                                                     (ASAH ) ASAHI KASEI KK
                                                                                                                        WPI; 2004-122214/12.
P-PSDB; ADI26143.
                                                                                                                                                                                                                                    diabetes and cancer.
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Matches 1630; Conserv
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                                                                                                                                                                                                                         GAATGTTAGAATATGATCCAACTCAAAGAATTACCTTGGATGAAGCATTGCAGCATCCTT
                                                                                                                                                                                                                                                                                          1421 TCTTTGACTTATTAAAAAAGAAATGAAAAGGAATCAGTGGTCTTACTATATACTTCTCT
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                                                                                                                              TGAAGGAATTTATGCTTTGTCATGATGAAGAACATGAGAAACTGTTTGACCTGGTTCGAA
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; 2002US-0385912P.
; 2002JP-00377326.
; 2002US-0436467P.
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06-JUN-2002;
26-DEC-2002;
27-DEC-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention is related to the isolation of a ligand known as beacon from the Israeli sand rat. Beacon is associated with the regulation of energy balance, and the protein, its coding sequence and analogues can be used in the treatment of diabetes, obesity, anorexia, energy imbalance, metabolic syndrome, dyslipidaemia, hypertension and insulin resistance. In addition, they can be used in agriculture to produce leaner animals
                                                       1661 GAAATTACCATTTTTAAAAACCTTTGAAAATATCCTTTGTGTCCAGTGATAAAATGTGTGATTG
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GAAATTACCATTTTAAATACCTTTGAAATATCCTTTGTGTCCAGTGATAAATGTGATTG
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Pred. No. 4.9e-271;
3; Mismatches 14;
                                                                                                                                                                                                                                                                                                             Human beacon partial coding sequence SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
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                                                                                                                                                                                                                       standard; DNA; 1323
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Best Local Similarity 98.9
Matches 1309; Conservative
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human; ds.
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                              TAGGCCGTTACCGTGAAGCAGCTCGTTCAGAAATCCAAGTATTAGAGCACTTAAATAGTA
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The invention relates to a method of identifying compounds that influence fat cell number or size comprising providing a cell that expresses a gene and an agent, exposing the cell to the agent and identifying fat cell number or size relative to cells not exposed to the agent. The method also comprises providing an expression vector and an agent, exposing the vector to the agent, detecting a change in expression of the gene calative to expression of the gene in an expression vector not exposed to the agent, treating a subject with the agent and identifying fat cell number or size in the subject comprises an antisense of igonomoleotide. The subject comprises a mammal, preferably a human. The colypeptide to the agent, detecting binding of the agent to the colypeptide to the agent, detecting binding of the agent to the colypeptide or a change in an activity of the polypeptide, treating a subject comprises an antibody, A method of regulating fat cell number or size comprises an antibody, A method of regulating fat cell number or size comprises providing a subject containing the subject containing the subject or number contained as useful for identifying containing the subject containing the subject or number or size in the expression of a gene, and treating the subject containing the subject containing the subject containing and an account of a gene, and treating the subject containing the subject contains the 
                                    or size for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying compounds that influence fat cell number or size for treating or preventing obesity or diabetes by exposing the cell to the agent and identifying fat cell number or size relative to cells not exposed to the
            influence fat cell number or size, for preparing a composition for treating or preventing obesity or diabetes. This sequence represents human cDNA used in the scope of the invention.
                                                                                                                                                                                                                                                                                                                                                   number; fat cell size; obesity; diabetes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a purified protein promoting signal transducer and activator of transcription 6 activation (STAT6). The protein is useful for the producing an antibody, which involves administering the protein or its epitope-bearing fragments to a non-human animal as an antigen. The nucleic acid is useful for diagnosing a disease or susceptibility to a disease related to expression or activity of the protein. A transformant expressing the protein is useful for screening compounds which inhibit or promote STAT6 activation. A transformant
                                                        AGCTAGATTAGGGATGAACACAGTTCTGCTGGTAGATATGTTAGGAGACGCTGCAAACCGT
                                                                                                                 TGAAGGAATTTATGCTTTGTCATGAAGAACATGAGAAACTGTTTGACCTGGTTCGAA
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                                                                                                                                                            GAATGTTAGAATATGATCCAACTCAAAGAATTACCTTGGATGAAGCATTGCAGCATCCTT
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                                                                                                                                                                                                                                                                                                                                                                                                             Human cDNA encoding protein that promotes STAT6 activation #53
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2002UP-0436467P.
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                                                                                                                                                                                                                                    Sequence 1881 BP; 570 A; 344 C; 450 G; 517 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                               56.6%; Score 1277.4; DB 12; Lengt
87.9%; Pred. No. 5.6e-266;
ive 0; Mismatches 192; Indels
 protein is useful for producing
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                                                                                                                                                                                                                                                                      1466 TATGGTCTTGATAATGCATTAGAAAAATTAAAATTTAATTTTTCTTTTTGAAATTACCATT
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806 ATATCAAAGTTGTTGACTTTGGAAGTGCAACGTATGATGATGAACATCACAGTACTTTGG
                                       369 ATATCAAAGTTGTTGACTTTGGAAGTGCAACGTATGATGATGAAGAACATCACAGTACTTTGG
                                                                                                                     429 TGTCTACCCGGCACTACAGAGCTCCCGAGGTCATTTTGGCTTTAGGTTGGTCTCAGCCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to the isolation of genes AAC59277-C59325 encoding 49 human secreted proteins AAB33718-B33764. The genes can be used to generate fusion proteins by linking to the gene for the human isolated to generate fusion proteins by linking to the gene for the human cancer immunoglobulin G FC portion (SEQIDI) for increasing the stability of the fusion protein as compared to the human protein only. The genes and conditions, e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic candis, proteins, antibodies and (ant) agonists are useful in the clasmosts, proteins, antibodies and (ant) agonists are useful in the clasmosts, and other cancers of the adrenal gland, bone, bone in marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addision's disease, allergies, autoimmune haemolytic ansemnia, autoimmune thyroiditis, dispetes mellitus, Crohn's disease, and the caractive colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               505
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                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid molecules encoding human secreted proteins, used in preventing, treating or ameliorating a disorder.
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Pred. No. 4.6e-246;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 349-350; 410pp; English.
                                                                                                                                                                                                                                                                      Komatsoulis G;
                                                                                                                       16-MAR-2000; 2000WO-US006765.
                                                                                                                                                              99US-0126051P.
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  Ното варіепв.
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1042 TGTAATTGTTGAACGGGTGATTATTATTAACTCTAGATAAGCAGGTACTAGAAACCAAAA 1101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a composition comprising a plurality of CDNAs for detecting the altered expression of genes in an immunological cordetecting the altered expression of genes in an immunological cresponse. The invention also relates to a method of diagnosing or monitoring the treatment of an immunopathological condition in a sample, comparising obtaining nucleic acids from a sample, contacting the nucleic acids of the sample with an array comprising the plurality of cDNAs under conditions to form one or more hybridisation complexes and comparing the levels of the detected in a non-diseased sample, where an altered level of the detected hybridisation complexes correlates with the presence of an immunopathological condition. Also disclosed are an expression profile comprising a microarray and a plurality of detectable complexes and a comparing a plurality of polymuclectide probes. The cDNAs are useful as hybridisable array elements in a microarray for monitoring the diagnosis of an immunopathology, such as Crohn's disease, asthma, culcerative colitis, hypercosinophila, irritable bowel syndrome, osteoarthris, rheumatoid arrhritis or acute monocytic leukaemia, and in identifying agents for the treatment of the diseases. The microarray may also be used in drug discovery and development, toxicological and carcinogenicity studies, forensics or pharmacogenomics. The composition of a subpopulation of a mixth composition of a my part of may also be used in drug discovery and development, toxicological and carcinogenic fragments. This sequence capresents a human cDNA of the invention. Note: The sequence data for this patent did not form part of the printined specification but was obtained in electronic format directly form.
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                                                                                                                                                                                                                                                                                                                                                                                    A composition comprising a plurality of cDNAs, useful for detecting altered expression of genes in an immunological response or for diagnosing and treating an immunopathology, e.g. Crohn's disease, asthma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  442 ACAGITCTGCTGGTAGATATGTTAGGAGACGCTGCAAACCGTTGAAGGAATTTATGCTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1, SEQ ID NO 699; 50pp; English
                                                                                                                                                                                                                                                                                            Seilhamer JJ;
                                                                                                                                              98US-00023655.
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Matches 1191; Conservative
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1049 ACATGATTCAGAAAACAAGAAAACGCAAGTATTTTCACCATAACCAGCTAGATTGGGATG 1108
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                                                                                           TTGAACTACTGGGACTTAGTACTTACGATTTTCATTAAAGAAAACAGCTTTCTGCCATTTC
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                                                          AAGCAGCTCGTTCAGAAATCCAAGTATTAGAGCACTTAAATAGTACTGATCCCAATAGTG
                                                                                                                                                                          TCTTCCGATGTGTCCAGATGCTAGAATGGTTTGATCATCATGGTCATGTTTGTATTGTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a purified protein promoting signal transducer and activator of transcription 6 activation (STAT6). The protein is useful for the producing an antibody, which involves administering the protein or its epitope-bearing fragments to a non-human animal as an antigen. The nucleic acid is useful for diagnosing a disease or succeptibility to a disease related to expression or activity of the protein. A transformant expressing the protein is useful for screening compounds which inhibit or promote STAT6 activation. A transformant expressing the protein is useful for proteining a pharmaceutical composition. Compositions, antibodies and antisense molecules are useful for the treating a disease associated with STAT6 activation such as allowed the protein is useful for acneers. Compositions are useful for treating diseases. Inflammation, autoimmune disease, diabetes, hyperlipidaemia, inflammation, autoimmune disease, diabetes, byperlipidaemia, infections disease and cancers. Compositions are useful for treating disease associated with STAT6 activation and/or prevention of Thi hyperactive diseases. Compositions are also useful in rheumatoid allergic thinitis, ischaemic heart diseases, subarachnoid haemorrhage, viral hepatitis and AIDS. The protein has efficient promoting STAT6 compounds for treating and proventing disease associated with excessive the protein or nucleic acid is effectively useful for screening compounds for treating and preventing disease associated with excessive the protein or nucleic acid is effectively useful for screening compounds for treating and preventing disease associated with excessive the protein and all protein and all protein and proventing disease associated with excessive the protein or nucleic acid is effectively useful for screening compounds for treating and preventing disease associated with excessive the protein and proventing disease associated with excessive the protein and proventing disease associated with excessive the protein and proventing states.
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                                                                                                                                                                       systemic lupus erythematosus; sepsis; asthma; allergic rhinitis;
ischaemic heart disease; subarachnoid haemorrhage; viral hepatitis; AIDS.
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                                                          activator of transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New signal transducer and activator of transcription 6 activation promoting purified protein, for diagnosing and treating disease associated with activation/inhibition of transcription factor e.g.
                                                    ss; gene; human; signal transducer and activator of transcription STAT6; immunogen; STAT6 imanusquen; STAT6 autoimmune disease; diabetes; hyperlipidaemia; infection; cancer; Th1 hyperactive disease; rheumatoid arthritis; osteoarthritis;
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  encoding protein that promotes STAT6 activation #55.
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Pred. No. 1e-231;
); Mismatches 129; Indels
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2003JP-00137505.
2003US-0470836P.
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2002JP-00377326.
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Best Local Similarity 90.2%;
Matches 1191; Conservative
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human cDNA enc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-DEC-2002;
27-DEC-2002;
15-MAY-2003;
16-MAY-2003;
                                                                                                                                                                                                                                                         Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                      18-DEC-2003
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Pred. No. 4.5e-227; 0; Mismatches 118;

90.8%;

Best Local Similarity 90.8 Matches 1168; Conservative

220 133 280 193 340 253 400

74 ACGAATACAGGAATGACTACTGTGAAGGATATGTTCCTAGACATTATCACAGAGACATTG

134 AAAGCGGGTATCGAATCCACTGCAGTAAATCTTCAGTCCGCAGCAGGAGAAGCAGTCCTA

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GTCACTATTTAGAAGCAAGATGCTTGAATGAGAGAGATTATCGGGACCGGAGATACATTG

GTCATTATTTAGAAGCAAGGTCCTTGAATGAGCGAGATTATCGGGACCGGAGATACGTTG

AAAGGAAGCGCAATAGACACTGTTCAAGTCAGTCACGTTCGAAGAGCCACCGAAGGA AGAGAAAGCGTAATAGACCCTGTGCAAGTCATCAGTCGCATTCGAAGAGCCACCGAAGGA AAAGATCCAGGAGTATAGAGGATGAGGAGGGTCACCTGATCTGTCAAAGTGGAGACG

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<u> AAAGATCCAGGAGTATAGAGGATGATGAGGAGGGTCACCTGATCTGTCAAAGTGGAGACG</u>

TTCTAAGAGCAAGATATGAAATCGTGGACACTTTAGGTGAAGGAGCCTTTGGCAAAGTTG TAGAGTGCATTGATCATGGCATGGCATGCATGTAGCAGTGAAAAATCGTAAAAAATG 521 TAGAGTGCATTGATCACGGCATGGATGGATGCTTACATGTAGCAGTGAAAATTGTAAAAATG

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TAGGCCGTTACCGTGAAGCAGCTCGTTCAGAAATCCAAGTATTAGAGCACTTAAATAGTA CTGATCCCAATAGTGTCTTCCGATGTCCAGATGCTAGAATGGTTTGATCATCATGGTC ATGITIGIATIGIGITIGAACTACTGGGACTTAGTACTTACGATTTCATTAAAGAAAACA

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       1589 CATGGAGGTCACCTCTGAAGTGATTTTTTTGAGTAAAAGGAAATCTTGACTACTTTATA 1648
                                        CATGGAGGTCACCTCTGAAGTGATTTTTTTTGAGTAAAAGGAAATCTTGACTACTTTAAA 1864
                                                                                                                                                                                                                                                                                                                          Identifying compounds that influence fat cell number or size for treating or preventing obesity or diabetes by exposing the cell to the agent and identifying fat cell number or size relative to cells not exposed to the
Mouse, gene, ss; fat cell number; fat cell size, obesity, diabetes; anorectic; antidiabetic.
                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 138; 275pp; English.
                                                                                        BP.
                                                                                        AD007812 standard; cDNA; 1446
                                                                                                                                                                                                                                   09-OCT-2002; 2002US-00267502
                                                                                                                                                                                                                                                   09-OCT-2002; 2002US-00267502
                                                                                                                         (first entry)
                                                                                                                                        Mouse polynucleotide #36.
                                                                                                                                                                                                                                                                   (LIFE-) LIFE SCI DEV
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P-PSDB; ADO08029.
                                                                                                                                                                                                                                                                                    Galant R;
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                                                                                                                                                                                                                   15-APR-2004
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                                                                                                         AD007812;
                                                                                                                                                                                   Mus sp.
                                                                                                                                                                                                                                                                                    Kim J,
                                                                                                                                                                                                                                                                                                                                                    agent
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The invention relates to a method of identifying compounds that influence fat cell number or size comprising providing a cell that expresses a gene and an agent, exposing the cell to the agent and identifying fat cell number or size relative to cells not exposed to the agent. The method also comprises providing a change in expression of the gene call the agent and identifying fat cell relative to expression of the gene in an expression vector not exposed to the agent, treating a subject. The agent and identifying fat cell number or size in the subject with the agent comprises an antisense of ilgonucleotide. The subject comprises an ammal, preferably a human. The oligonucleotide to the agent, detecting binding of the agent to the comprises providing a polypeptide and an agent, exposing the polypeptide to the agent, detecting binding of the agent to the agent and identifying fat cell number or size in the subject or a change in an activity of the polypeptide, treating a comprises providing a subject containing fat cells and an agent that changes the expression of a gene, and treating the subject containing fat cells and an agent that changes the expression of a gene, and treating the subject with the agent under conditions so that fat cell size or number in the subject is altered. The method is useful for identifying compounds that influence fat cell number or size, for preparing a composition for treating or preventing obselfy or diabetes. This sequence represents
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Length 1446;

48.6%; Score 1097.2; DB 12;

Query Match

Sequence 1446 BP; 461 A; 272 C; 352 G; 361 T; 0 U; 0 Other;

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                         TAAATTTTTTACATCATAAATTAACCCATACAGATCTGAAGCCTGAAAATATTTTGT
                                                    TAAATTTTTTTACATCATAAATTAACACACACGCACCTAAAACCTGAAAATATTTTAT
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GACCCATCCCAGCACATATGATCCAGAAGACAAAACGCAAGTATTTCCACCATAACC 1240
                                                                                                                                                                                                                                                                                                                                                                                       Human; kinase protein; enzyme; cytostatic; osteopathic; gene expression; colon-moderately differentiated adenocarcinoma; chromosome mapping; gene; drug screening; therapeutic; gene therapy; tissue typing; chromosome 5; bone osteosarcoma; single nucleotide polymorphism; SNP; ds.
                                        1301 TAAAGGAATTTATGCTGTGTCATGACGAAGAGCATGAGAAAGCTGTTTGACCTGGTTCGAA
                                                                                                                                                   GAATGTTGGAGTATGACCCAGCGAGAAGGATCACCTTGGATGAAGCATTGCAGCACCCTT
                                                                            TGAAGGAATTTATGCTTTGTCATGATGAAGAACATGAGAAACTGTTTGACCTGGTTCGAA
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The invention relates to isolated human kinase proteins and mucleic acid and peptide sequences can be used as models for the development of human therapeutic targets, aid in the identification of therapeutic proteins and serve as targets for the development of human therapeutic proteins and serve as targets for the development of human that express the kinase. The mucleic acids are useful as probes or primers, in constructing recombinant vectors, for expressing antigenic portions of the proteins, chromosome mapping, drug screening, testing an individual for a genotype, and for gene therapy in patients containing cells that are aberrant in kinase gene expression. The proteins may be used in drug screening assays, in the identification of compounds that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New human kinase proteins and nucleic acids, useful in drug screening assays, identifying modulators of kinase activity or treating disorders characterized by absence or unwanted expression of the protein.
                                                                                                                                                                                                                                                                                    standard name= "Single nucleotide polymorphism" 3438. .13520
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/standard_name= "Single nucleotide polymorphism"
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6595. .17962
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19-MAR-2001; 2001US-00810671.
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analysis, in treating disorders characterised by an absence or unwanted expression of the protein (bone osteosarcoma, or colon-moderately differentiated adenocarcinoma), and in generating antibodies specific for the peptides. Such antibodies can be used to detect the protein in situ, in vitro, or in cell lysate or supernatant, to isolate and purify the protein from host cells, pharmacogenomic analysis, tissue typing, and in inhibiting protein function. The present sequence is human kinase protein gene located on chromosome 5
modulate, stimulate or inhibit kinase activity, in pharmacogenomic
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Sequence 21234 BP; 6065 A; 3772 C; 4258 G; 7139 T; 0 U; 0 Other;

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1 21234;	0
Length 2	Indels 0; Gaps
3 6;	0;
Score 1097; DE Pred. No. 1e-2	0; Mismatches
48.6%;	ative
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1276	18257	1336	18317
1217 IGTTAGAATATGAICCAACTCAAAGAATTACCTTGGATGAAGCATTGCAGCATCCTTTCT 1276	18198 IGTTAGAATATGATCCAACTCAAAGAATTACCTTGGATGAAGCATTGCAGCATCCTTTCT 18257	1277 TTGACTTATTAAAAAAAAAGAAATGAAATGGGAATCAGTGGTCTTACTATATACTTCTCTAGA 1336	18258 TICACITATIAAAAAGAAAIGAAAIGGGAAICGCGICCITACIAIAIATACITCITAGA 18317
121	1819	127	1825

Search completed: March 16, 2005, 09:01:21 Job time : 1200.6 secs

1277	1277 TIGACTIATTAAAAAAAAATGAAATGAAATGAGTGTGTGTGTGTTACTATATACTTCTCTAGA 1336	1336
18258	18258 TIGACTTATTABABABGBABATGBABATGBABTCAGTGGTCTTACTATATACTTCTCTAGA 18317	18317
1337	1337 AGAGATTACTTAAGACTGTGTCAGTCAACTAAACATTCTAATATTTTTTGTAAACATTAAA 1396	1396
18318		18377
1397	1397 ITATITIGIACAGITAAGIGIAAAIAITGIAIGITITIGIAICAAIAGCAIAAIIAACITG 1456	1456

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1397	1397 TIATITIGIACAGITAAGIGIAAATATIGIAIGITITIGIATACAATAGCATAATTAACTIG 1456	1456
18378	18378 TIATTITICHACAGITHAAGIGIAAAHATIGIAHGITITIGIAHCAATAGCATAATHAACITG 18437	18437
1457	1457 ITAAGCAAGTATGGTCTTGATAATGCATTAGAAAAATTAAAATTAATT	1516
18438	TTAAGCAAGTATGGTCTTGATAATGCATTAGAAAAATTAAAATTAATT	18497
1517	1517 ATTACCATTTTTAAATACCTTTGAAATATCCTTTGTGTCCAGTGATAAATGTGATGATC 1576	1576

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18558 TIGCCTITICIACATGAGGTCACCICTGAAGTGATTTTTTTTTT	18558
1577 TIGCCITITIGIACAIGGAGGICACCICTGAAGIGAITITITITIGAGIAAAAGGAAAICI'	1577
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1637	18618	1697	18678

_	1757 ACTAGAAACCAAAACTCAGAAAATGTTTACTGTTAGAATTCTATTAAATTTTAAGTGTTG 1816	1816
-S	18738 ACTAGAAACCCAAAACTCAGAAAATGTTTACTGTTAGAATTCTATTAAATTTTAAGTGTTG 18797	18797
TA-	1817 TATTCTTTTTCATTGGGTGATGTCAGGGTGATAACCAGACATTCATGGAAAGGCATGCAG 1876	1876
-£	18798 TATTCTTTTTCATTGGGTGATGTCAGGGTGATAACCAGACATTCATGGAAAGGCATGCAG 18857	18857
Ľ-	1877 TITGICCATIGIGACAGITITGITIAATAAAACCACATACACACTITTAATTAAGATTAAAA 1936	1936
-Ľ	18858 TITCICCATTGTCACAGTTTGTTTAATAAACCACATACACACTTTATTTA	18917

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1996	18977	2056
1937 TCTAACTGGAAAGTCAGCTTGGAAATGGACATTTCCAAGTATGTTTGGTGAGTCACAGA 1996	18918 TCTAACTGGAAAGTCAGCTTGGAAAATGGACATTTCCAAGTATGTTTGGTGAGTCACAGA 18977	1997 TATAAAAATAGAAATTCTGATGAGAGGTTTCAGTTTTTAATACCAAGTCCTTAGGAGTCT 2056
1937	18918	1997

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AX534244 Sequence
AX39282 Sequence
AC022097 Homo sapi
AC022096 Homo sapi
BC002220 Mus muscu
CQ718110 Sequence
AY653308 Mus muscu
BC079006 Rattus no
BX931976 Gallus ga
AB056421 Macaca fa
CQ715616 Sequence
BC031549 Homo sapi
L29219 Homo sapien
X57186 Mouse clk m
M38381 Mouse serin
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BX936001 Gallus ga
BX929601 Gallus ga
BX929601 Gallus ga
L29222 Homo sapien
MS9287 Human prote
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BY179987 sgmul0751
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1 (bases 1 to 2354)

1 (bases 1 to 2354)

1 Ye, J., Ketchum, K.A., Di Francesco, V. and Beasley, B.M.

1 Isolated human kinase proteins, nucleic acid molecules encoding human kinase proteins, and uses thereof Patent: US 6455291-A 1 24-SEP-2002;

Location/Qualifiers
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Sequence 1 from patent US 6455291.
AR232168
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BC031549
HUMCLK1B
MMCLKMRNA
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HUMCLK1A
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11   AGCOLOGORAGOANGACOLOGOGOATATAGAGGATCATCAGAGGATCATCTCTCTT   21   CAMATTCGAGACCTCTCACACCTCTCTCTCT   21   CAMATTCGAGACCTCTCACACCTCTCCTCAGAGCC   21   CAMATTCGAGACCTTCTCAGACCTTCTCCAGACCTTCTCTCTC	1201 GACCTGGTTCGAAGAATGTTAGAATATGATCCAACTGAAAGAATTACCTTGGATGAAGCA 1260

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432 ITTGGCAAAGTTGTAGAGTGCATTGATCATGGCATGGCAT					721 GAAAATATTTTGTTTGTGAAGTCTGACTATGTAGTCAAATATAATTCTAAAATGAAACGT 780 	781 GATGAACGCACACTGAAAAACACAGATATCAAAGTTGTTGACTTTGGAAGTGCAACGTAT 840 	841 GATGATGAACATCACAGTACTTTGGTGTCTACCCGGCACTACAGAGCTCCCGAGGTCATT 900	TIGGCTTIAGGITGGTCTCAGCCTIGTGATGTTTGAGCATAGGITGCATTCTTATTGAA TIGGCTTTAGGITGCTCCAGCCTTGTGATGTTTGAGCATAGGITGCATTCTTATTGAA TIGGCTTTAGGITGGTCTCAGCCTTGTGATGTTTGGAGCATAGGTTGCATTCTTATTGAA	961 TATTACCTIGGTTTCACAGICTTTCAGACTCAIGATAGTAAAGAGCACCIGGCAAIGAIG 1020 	1021 GPACGBALTATGGGCCCGTACCACAACACATGATTCAGAAAACAAGAAAACGCAAGTAT 1080	1092 GAACGAATATTAGGACCCATACCACAACACATGATTCAGAAACAGAAACAGAAAACGAGTAT 1151	TTTCACCATAACCAGCTAGATGAGGATGAACACAGTTCTGCTGGTAGATATGTTAGGAGA	CGCTGCAAACCGTTGAAGGAATTTATGCTTTGTCATGATGAAGAACATGAAAAACTGTTT 1	GACCTGGTTCGAAGAATGTTAGAATATGATCCAACTCAAAGAATTACCTTGGATGAAGCA 13		145	1381 TTTTGTAAACATTAAATTATTTTGTACAGTTAAGTGTAAATATTGTATGTTTTGTATCAA 1440 	1441 TAGCATAATTAACTTGTAAGCAAGTATGGTCTTGATAATGCATTAGAAAATTAAAATT 1500 
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/organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"	Query Match 100.0%; Score 2256; DB 6; Length 2354; Best Local Similarity 100.0%; Pred. No. 0; Matches 2256; Conservative 0; Mismatches 0; Indels 0; Gaps 0	Oy 1 GACACTCATCCCAGTCATTATTTAGAAGGTCCTTGAATGAGGAGATTATGGGGAC 60	Qy 61 CGGAGATACGTTGACGGAATACAGGAATGACTACTGTGAAGGATATGTTCCTAGACATTAT 120	QY         121         CACAGAGACATTGAAAGCGGGTATCGAATCCACTGCAGTAAATCTTCAGTCGGAGCAGG         180           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	QY         181 AGAAGCAGTCCTAAAAGGAAGCGCAATAGACACTGTTCAAGTCATCAGGTCAGGTTCGAAG         240           DD         252 AGAAGCAGTCCTAAAAGGAAGCGCAATAGACACTGTTCAAGTCATCAGTCACGTTCGAAG         311	QY         241 AGCCACCGAAGAAAAGATCCAGGAGTATAGAGGATGATGAGGAGGTCACCTGATCTGT 300	Oy 301 CAAAGTGGAGACGTTCTAAGAGCAAGATATGAAATCGTGGACACTTTGGGTGAAGGAGC 360	QY         361         TITGGCAAGTIGTAGAGTGCATTGATCATGGCATGGCATG	QY         421         ATCGTAAAAATGTAGGCCGTTACCGTGAAGCAGCTCGTTCAGAAATCCAAGTATTAGAG         480           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	OY 481 CACTTAAATAGTACTGATCCCAATAGTGTCTTCCGATGTGTCCAGATGCTAGAATGGTTT 540	QY         541 GATCATCATCATGTTTGTATTGTGTTTGAACTACTGGGACTTAGTACTTACGATTTC         600           bb         612 GATCATGCTTTGTATTGTGTTTGAACTACTGGGACTTAGTACTAGGATTTC         671	Oy 601 ATTAAAGAAAACAGCTTTCTGCCATTTCAAATTGACCACATCAGGCAGATGGCGTATCAG 660	OY 661 ATCTGCCAGTCAATAAATTTTTTACATCATAAATTAACCCATACAGATCTGAAGCCT 720  Db 732 ATCTGCCAGTCAATAAATTTTTTACATCATAAATTAACCCATACAGATCTGAAGCCT 791	QY 721 GAAAATATTTGTGAAGGTCTGACTAGGTGGAGTGAATATAATTCTAAAATGAAAGGT 780	OY 781 GATGAACGCACACTGAAAAACACAGATATCAAAGTTGTTGAAGTTGCAAGGTAT 840	OY 841 GATGATGAACATCACAGTACTTTGGTGTCTACCGGCACTACAGAGGTCCTT 900	Qy 901 TTGGCTTTAGGTTGGCCTTGTGATGTTTGGAGCATAGGTTGCATTCTTATTGAA 960
1501 AATTITCTTTTGAAATTACCATTTTTAAATACCTTTGAAATATCCTTTGTGTCCAGTG 1560 	1561 ATAAATGTGATTGATCTTGCCTTTTGTACATGGAGGTCACCTCTGAAGTGATTTTTTTT	1621 AGTAAAAGGAAATCTTGACTACTTTAFATTCTTAAAGGAATATTCTTTATATACTTCAAA 1680 	1681 TTTAGAACTTAAACTTTTTCTTCTGTAATTGTTGAACGGGTGATTATTAATAA 1740 	1741 CTCTAGATAAGCAGGTACTAGAAACCAAAACTCAGAAAATGTTTACTGTTAGAATTCTAT 1800 	1801 TAAATTTTAAGTGTTGTATTCTTTTTCATTGGGTGATGTCAGGGTGATAACCAGACATTC 1860 	1861 AIGGAAAGGCAIGCAGTTGTCCAITGTGACAGTTTGTTTAATAAAACCACATACACAT 1920 	1921 TTATTTAAGATTAAGATCTAACTGGAAAGTCAGCTTGGAAAATGGACATTTCCAAGTATG 1980 	1981 TTTGGTGAGTCACAGATATAAAATAGAAATTCTGATGAGAGGTTTCAGTTTTAATACC 2040 	2041 AAGTCCTTAGGAGTCTTAACATTGGCCAGCATCTGTTTATCAAATGACATAAATACGTAA 2100 	2101 ACCTATAAGAATTAAGTTTATTAATTAGGGAATTTATGTCTGTGATAATTCTTAGGGGAG 2160. 	2161 AAAGAGGATTTGATTGGAAAGCAGTTTGGGAAGAAGTGCTGCTGAAATTTCCAGAATTT 2220 	2221 AATTGATTGGTTACATAACTTTTGACTTCAGAAA 2256 		AX392827 ION Sequence 1 from Patent WO0216567. ON AX392827 AX392827.1 GI:19700923	S Homo sapiens (human) ISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	nammalla; butherla; Frimates; Catarrini; hominidae; homo. CE 1 Yan,C.C., Ye,J.C., Ketchum,K.A., di Francesco,V.C. and Beaslèy,E.M. Isolated human kinase proteins, nucleic acid molecules encoding	numan kinase proteins, and uses thereor AL Patent: WO 021657-A 1 28-FEB-2002; Applera Corporation (US) S Location/Qualifiers

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Db 2112 AAGTCCTTAGAGTTTATTATTAGCAGCATCTGTTATCAAATGACATAA 2171  Qy 2101 ACCTATAGAATTAAGTTTATTAATTAGGCAATTTATCAAATGACATAAAACGTAA 2171  Db 2172 ACCTATAAGAATTAAGTTTATTAATTAGGCAATTTATGTCTGAAATTCTTACGGGAG 2160  Qy 2161 AAAGAGGATTTGATTGGAAAGCAGTTTGGGAAAAGTGCTGCTGAAATTCTTACGGGAG 2231  Db 2232 AAAGAGGATTTGATTGGAAAGCAGTTTGGGAAGAAGTGCTGCTGAAATTTCCAGAATTT 2220  Qy 2221 AAATGATTGATTGGAAAGCAGTTTGGGAAGAAGTGCTGCTGAAATTT 2291  Db 2222 AATTGATTGGTTACATAAACTTTTTGACTTCAGAAA 2256  Db 2229 AATTGATTGGTTACATAAACTTTTTGACTTCAGAAA 2327	RESULT 5 AX056410 LOCUS AX056410 Sequence 54 from Patent W00073469. ACCESSION AX056410 AX06410 AX066410 AX064410 AX066410 AX06641	Query Match         90.8%; Score 2048; DB 6; Length 2488;           Best Local Similarity         95.9%; Pred. No. 0;           Matches 2148; Conservative         0; Mismatches         1; Indels         90; Gaps         1;           QY         14 GTCATTATTAGAAGCAAGTCCTTGAATGAGGAATTATCGGGACCGGAGTACGTTG         33         GTCATATTATAGAAGCAAGTCCTTGAATGAGGAATTATCGGGACCGGAGTACGTTG         39           QY         74 ACGAATACAAGACTCATGAAGGAATATCTTCAAGAATTATCACAGAGACATTG         39         ACGAATACAAGAATCACTGTGAAGGATATGTTCCTAAGACATTATCACAGAGACATTG         457           QY         134 AAAAGCAGGAATGACTACTGTGAAGAATATTCTAAGTCCCAAGAAACATTG         457           QY         134 AAAAGCAGGATATCGAATCCACTGCAAGTAAATCTTCAAGTCCGCAGCAGAAACACTCTA         193           QY         194 AAAAGGAGTATCGAATACAATCAAGTCAACTCAAGTCACTCGAAGAAACCTCTA         153           QY         194 AAAAGGAATACAATACAACTCTAAGTCAACTCAACTCAA	254 AAAGATCCAGGAGTATAGAGGATGATGAGGGGTCACCTGATCTGTCAAAGTGGAGGGTCACCTGATCTGTCAAAGTGGAGACG 562
	GACCTGGTTCGAAGAATGTTAGAATATGATCCAACTCAAAGAATTACCTTGGATGAAGGA  GACCTGGTTCGAAGAATGTTAGAATATGATCCAACTCAAAGAATTACCTTGGATGAAGGA  TTGCAGCATCCTTTCTTTCACTTATTAAAAAAGAATGAAATGGGAATCAGTGGTCTTAC  TTGCAGCATCCTTTCTTTGACTTATTAAAAAAGAATGAAATGGGAATCAGTGGTCTTAC  TATATACTTCTCTAGAAGAATTACTTAAAAAAGAATGGAAATGGGAATCAGTGGTCTTAC  TATATACTTCTCTAGAAGAATTACTTAAAAATGGTCAGTGGTCAACTAATAT  TTTTGTAAAATTATTTTTTTTTT	1572 ANITITICITITICADANITACCALITITADANIACCITICADANIACCITICALICANICANISTICANIA 1831 1561 ATANATGRATTGATCTTGCCTTTTGTACATGAGGGTCACCTCTGAGGTGATTTTTTTG 1620 1632 ATANATGGATTGATCTTGCCTTTTGTACATGAGGTCACCTCTGAGTGATTTTTTTT	1872 TAAAITTTAAGIGITTTTTTTTTTTTTTTTTTTTTTTTT

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Bandman,O., Hillman,J.L., Lal,P., Akerblom,I.E., Shah,P.,
Corley,N.C. and Guegler,K.J.
Protein Kinase molecules
Patent: US 5962222-A 9 05-OCT-1999;
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Schultz,J., Jones,T., Bork,P., Sheer,D., Blencke,S., Steyrer,S.,
Wellbrock,U., Bevec,D., Ullrich,A. and Wallaach,C.
Molecular characterization of a cDNA encoding functional human CLK4
kinase and localization to chromosome 5q35 [correction of 4q35]
Genomics 71 (3), 368-370 (2001)
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/db_xref="taxon:9606"
/chromosome="4"
/map="4435"
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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	RESULT 10 BC063116 LOCUS DEFINITION Homo sapiens CDC-like kinase 4, mRNA (cDNA clone INAGE:30324121), DEFINITION Homo sapiens CDC-like kinase 4, mRNA (cDNA clone INAGE:30324121), DETINITION Homo sapiens (DOCOSTICE (CONTINUED CONTINUED C	Altechul, S.F., Zeeberg, B., Buetow, K.H., Schaeter, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Uddin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, A.P., McKarn, R.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettemson, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Butfard, G.G., Blakesley, R.W., Touchman, J.W., Green, R.D., Dickson, M.C., Rodriguez, A.C., Gimwood, J., Schmutz, J., Myers, R.M., Schentch, A., Schein, J.E., Jones, S.J. and Marra, M.B., Schent, B.D. E., Schmutz, J., and Marra, M.B., Schent, J. Schmatz, J., and Marra, M.B., Schmatz, J., and Marra, J., and J. Schmatz, J., and Marra, J., and J. J., and	K BUK K	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL) DNA Sequencing by: Genome Sequence Centre,  BC Cancer Agency, Vancouver, BC, Canada  Info@Dogsc.bc.ca  Steven Jones, Jennifer Agano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Haiao, Martin Kzzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Lilsa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,
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2 (bases 1 to 1446)

Park,J., Rolfe,A., Hu,Y., Shen,B., Vannberg,F., Moreira,D.,
Kelley,T., Zuo,D., Raphael,J., Baqui,M., Jepson,D., Harlow,E.,
LaBaer,J., and Brizuela,L.
Direct Submission
Submitted (02-JUL-2003) Biological Chemistry and Molecular
Pharmacology, Harvard Institute of Proteomics, 320 Charles St.,
Cambridge, Ma 02141-2023, USA
This CDS clone is a part of a collection of human full-length
expression clones generated by Harvard Institute of Proteomics.
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Park, J., Rolfs, A., Hu, Y., Shen, B., Vannberg, F., Moreira, D.,
Kelley, T., Zuo, D., Raphael, J., Baqui, M., Jepson, D., Harlow, E.,
LaBaer, J. and Brizuela, L.
Cloning of human full-length CDS FLEXGene kinases in
recombinational vector system
                      ACACATGATTCAGAAAAACGAAAAACGCAAGTATTTTCACCATAACCAGGTAGATTGGGA
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                                                  Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAL Plate: 51 Row: a Column: 9 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 10190705. Location/Qualifiers
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                                                                                                                                                                             /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="type="mRNA"
/clone="IMAGE:30324121"
/tissue_type="Skin and meninges pool- skin, dura matter,
pia matter, choroid plexus."
/clone_lib="WIH MGC_186"
/lab_host="PH108"
Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy
George Yang, Scott Zuyderduyn, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGTCTTCCGATGTCCCAGATGCTAGAATGGTTTGATCATCATGGTCATGTTTGTATTGT
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                                                                                                                                                                                                                                                                                                                                                                                     Score 1318.4; DB 9;
Pred. No. 1.6e-234;
0; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                /note="Vector: pDNR-LIB"
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llarity 99.2%;
Conservative (
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Matches 1325;
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (Dases I to 1914)
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
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Mus musculus CDC like kinase 4, mRNA (cDNA clone MGC:13871
IMAGE:3382920), complete cds.
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                                 ATGTTTGTATTGTGTTTGAACTACTGGGACTTAGTACTTACGATTTCATTAAAGAAAACA
                                                                                                 GCTTTCTGCCATTTCAAATTGACCACATCAGGCAGATGGCGTATCAGATCTGCCAGTCAA
                                                                                                                                                               GCTTTCTGCCATTCAAATTGACCACATGCGCAGAGGCGCAGATGGCGTATCAGATCTGCCAGATCAA
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Mus musculus
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BC012675.1 GI:15215130
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AUTHORS
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Each CDS has been cloned without stop-codon (to allow fusion with C-terminal tag). The CDS has been directionally cloned using BD In-Fusion(TM) cloning system between the Sall and HindIII sites of the pDNR-Dual vector. Additional sequences in the clone: 'ACC' after Sall site and before 'ATG' to provide Kozak consensus sequence; 'GG' after last codon and before HindIII site to maintain
                                                                                                                                                                                                                                                                                                                                                                                                                                 / db xref="01.33304091"
/ db xref="01.33304091"
/ translation="WRHSKRTHCPDWDSRESWGHESYRGSHKKKRESHSSTOENRHCK
PHHOPKESDCHYLEARSLINENDYDRRYUDEYRNDYCEGYVPRHYHDIESGYRIHCS
KSSYRSRRSS PRIKKNHCSSHORSRESHRKKRSESIEDDEEGHLICOSGDYLARAKYE
IVDTLGEGAFGKVVECIDHGMDGMHVAVKIVKNVGRYREARSEIQVLEHLNSTDPNS
YRCVQMLEMPEDHHGHYCIVPELLGLSTYDFIKENSFLPFQIDHIRQYAYQICOSINF
LHHNKLTHTDLKPENILLFVKSDYVVKYNSKMKRDERTLKNYDIKVVDFGSATYDDEHH
STLVSSTRYRAAREVILLALGWSOPCDWSIGCILIEYYLGFTVRQTHDSKEHLAMMERI
LGPIPQHMIQKTRKRKYFHHNQLDMDEHSSAGRYVRRRCKFLKEFMLCHDEEHEKLFD
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                                                                                                                                                                                                                /tissue type="placenta and brain"
/clone_lib="First strand cDNA from placenta and brain"
/lab_host="DH5alpha T1 resistant"
/note="Vector: pDNR-Dual"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTCTAAGAGCAAGATATGAAATCGTGGACACTTTGGGTGAAGGAGCCTTTGGCAAAGTTG
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100.0%; Pred. No. 4.4e-228;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LVRRMLEYDPTQRITLDEALQHPFFDLLKKKL
                                                                                                                                1. .1446
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                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                               1. .>1446
/gene="CLK4"
                                                                                                                                                                                                                                                                                                                  .>1446
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                                                                                                    reading frame.
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Matches 1284;
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Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S. I., Wang, J., Hsleh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blackeley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalbka, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="MGI:109851"
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IVDTIGEGGAFGKVVECIDHGMDGLHVAVKIVKNVGRYREAARSEIQVLEHLNSTDPNS
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Series: IRAK Plate: 18 Row: c Column: 18
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 6671765.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="MGC:13871 IMAGE:3982920"
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/clone lib="MCI CGAP_Lu29"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (15-MG-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anuradha
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anurac
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Institute for Systems Biology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIH-MGC Project URL: http://mgc.nci.nih.gov
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protein id="AAH12675.1"
db_xref="GI:15215131"
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/db_xref="LocusID:12750"
/db_xref="MGI:1098551"
1017. .1546
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human and mouse cDNA
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AUTHORS
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JOURNAL
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FEATURES

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LHHNKÄTHTDLKPENILFVKSDYVVKYNSKMKRDERTLKMTDIKVVÖFGSÄTYÖDEHH
STAVSTRHYRABEVILALGMSQPCDVNSIGCILIEYYLGFTVRQTHDSKEHLAMMERI
LGPIPAHMIQKTRKRYFHHNQLDMDEHSSAGRYVRRRCKPLKEFMLCHDEEHEKLFD
LVRRMLEYDPARRITLDEALQHPFFDLLKRK
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VFRCVQMLEWFDHHGHVCIVFELLGLSTYDFIKENSFLPFQIDHIRQMAYQICQSINF
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                                                                                                                                                                                                                         321 ATGAATACAGAAATGACTACTGCGAAGGATATGTTCCAAGACATTACCATAGAGACGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    501 AAAGATCCAGGAGTATAGAGGATGATGAGGAGGGTCACCTGATCTGTCAAAGTGGAGAGG
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                                                                                                                                                                                                                                                                         74 ACGAATACAGGAATGACTACTGTGAAGGATATGTTCCTAGACATTATCACAGAGACATTG
                                                                                                                                                                                                                                                                                                                                                AAAGCGGGTATCGAATCCACTGCAGTAAATCTTCAGTCCGCAGCAGGAGAAGCAGTCCTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 374 TAGAGTGCATTGATCATGGCATGGATGGCATGTAGCAGTGAAAAATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                861 GTTTTCTGCCATTTCAAATTGATCACATCAGGCAAATGGCTTATCAGATCTGCCAGTCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       921 TABATTTTTTACATCATAATAAATTAACACACGCGACCTAAAACCTGAAAATATTTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTGTGAAGTCTGACTATGTAGTCAAATATAATTCTAAAATGAAACGTGATGAACGCACAC
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                                                                                                                                                                  Gaps
                                                                                                                          56.6%; Score 1277.6; DB 10; Length 1914; larity 87.5%; Pred. No. 6.5e-227; Conservative 0; Mismatches 200; Indels 3; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        314 TTCTAAGAGCAAGATATGAAATCGTGGACACTTTGGGTGAAGGAGCCT
                                                                                                                        Query Match
Best Local Similarity
Matches 1418; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                             441
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/db_xref="G1:40881305"
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VFRCVQMLEWFDHHGHVCIVFELLGLSTYDFIKENSFLPFQIDHIRQMAYQICQSINF
LHHNKLTHPDLKFENILFWKSDYVKXNSKMKEDERTLKNTDIKVDFGSATYDDEHH
STLYSTRHYRAPEVILALGWSQPCDVWSIGCILIEYLGFTVFQTHDSKEHLAMMERI
LGPIPAHMIQKTRKRYFHHNQLDWDEHSSGRYVERRCKPLKEFMLCHDEEHEKLFD
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Pred. No. 7.1e-227;
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note="unnamed protein product"
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                            GACCCATACCACACACACATGATTCAGAAAACAAGAAAACGCAAGTATTTTCACCATAACC
                                                                                                                                                                                                                                                                         GGTCTCAGCCTTGTGATGTTTGGAGCATAGGCTGCATTCTTATTGAGTACTACCTTGGGT
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                             TCACAGTCTTTCAGACTCATGATAGTAAAGAGCACCTGGCAATGATGGAACGAATATTAG
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/db_xref="taxon:10090"
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PD 26-NOV-2002
PF 16-MAR-2000 JP 2000606614
PR 33-MAR-1999 US 60/169906 PI
CRAIG A ROSEN,STEVEN M RUBEN,GEORGE KOMATSOULIS PC
CLANIS/09,A61R35/36,A61R38/00,A61R48/00,A61P17/02,A61P25/14, PC
A61P25/16,
PC CLANIS/16,
PC CLANI/15, R61P25/24,A61P25/28,A61P29/00,C07K14/47,C07K16/18,PC
PC CLANI/15, PC CLANI/1
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/organism="Homo sapiens"
/mol_type="genomic DNA"
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1. (baese 1 to 122)

Rosen, C.A., Ruben, S.M. and Komatsoulis, G.
49 human secreted proteins
Patent: JP 2002539776-A 16 26-NOV-2002;
HUMAN GENOME SCIENCES INC
OS Homo sapiens (human)
PN JP 2002539776-A/16
                                                                                     GGTCTCAGCCTTGTGATGTTTGGAGCATAGGCTGCATTCTTATTGAGTACTACTTGGGT
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JP 2002539776-A/16.
Homo sapiens (human)
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1 (bass 1 to 1456)

1 (bass 1 to 1456)

Cocks, B.G., Stuart,S.G. and Seilhamer,J.J.

Compositions for the detection of blood cell and immunological response gene expression

Patent: US 6607879-A 699 19-AUG-2003;

Location/Qualifiers
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                         TTTGGAGCATAGGTTGCATTCTTATTGAATATTACCTTGGTTTCACAGTCTTTCAGACTC
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0; Mismatches 3; Indels 1;
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/organism="unknown"
/wol_type="genomic DNA"
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model	4 429 17.8 1457 2 T14577 5 419 17.4 1209 2 T14357 6 406 5 16 9 477 2 T11720	n kinase Yak omain-intera
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ıń	4 338.5 14.0 523 2 14/560 5 334 13.9 361 2 T51943	serine protein Kin mitogen-activated
residues	ALIGNMENTS	
chosen parameters: 283416		***
	MESULI 1 \$3541 protein kinase clkl (EC 2.7.1) - human	
0% 100% 45 summaries	C; Species: Homio Bapiens (man) C; Date: 15-Unio 1995 #sequence_revision 01-Sep-1995 #text_change C; Accession: 853641 R; Hanes, J.; von der Kammer, H.; Klaudiny, J.; Scheit, K.H.	09-Jul-2004
	J. Mol. Blod. 244, 665-672, 1994 A.Title: Characterization by cDNA cloning of two new human protein kinases A.Reference number: S53637, MUID:95082033, PMID:7990150 A.Accession: S53641 A.Status: nucleic acid sequence not shown A.Molecule type: mRNA	n kinases. Evidence by t
results predicted by chance to have a . to the score of the result being printed, of the total score distribution.	B:L29219; NID:g632963; lk1; protein kinase hom sphotransferase logy «KIN»	PIDN:AAA61480.1; PID:g632968 ology
SUMMARIES Description	Query Match 78.3%; Score 1887; DB 2; Length 48 Best Local Similarity 82.1%; Pred. No. 2.1e-83; Matches 352; Conservative 30; Mismatches 45; Indels	2; Gaps 2;
protein kinase clk protein kinase STY protein kinase (EC	QY         18 SHYLEARSLNERDYRDRRYVDEYRNDYCEGYVPRHYHRDIESGYRIHCSKSSVRSBRSSP	SVRSRRSSP 77               SGRSGRSSY 113
procein kinase Cik procein kinase Clk procein kinase Clk procein kinase Dar	Qy 78 KRK-RNRHCSSH-QSRSKSHRRKRSRSIEDDEEGHLICQSGDVLRARYEIVDTLGEGAFG	OTLGEGAFG 135           OTLGEGAFG 173
probable protein k protein kinase STY protein kinase AFC protein kinase PK1	QY         136 KVVECIDHGMDGMHVAVKIVKNVGRYREAARSEIQVLEHLNSTDPNSVFRCVQMLEWFDH           D         174 KVVECIDHKAGGRHVAVKIVKNVDRYCEAARSEIQVLEHLNTTDPNSTFRCVQMLEWFEH	VQMLEWFDH 195             VQMLEWFEH 233
protein kinase, 54 protein kinase AME lammer kinase homo probable protein k	Qy 196 HGHVCIVFELLGLSTYDFIKENSFLPFQIDHIRQMAYQICQSINPLHHNKLTHTDLKPEN	HTDLKPEN 255
probable serine/th probable serine-th protein kinase - f hypothetical prote	QY 256 ILFVKSDYVVKYNSKMKBERTLKNTDIKVVDFGSATYDDEHHSTLVSTRHYRAPEVILA	RAPEVILA 315
hypothetical prote protein kinase DYR protein kinase DYR hypothetical prote	OY 316 LGWSQPCDVWSIGCILIEYYLGFTVFQTHDSKEHLAMMERILGPIPQHMIQKTRKRKYFH	KTRKRKYFH 375            KTRKRKYFH 413
hypothetical prote Down-syndrome-crit homeodomain-intera probable, protein k	Qy 376 HNQLDWDEHSSAGRYVRRRCKPLKEFMLCHDEEHEKLFDLVRRMLEYDPTQRITLDEALO  ::	XITLDEALO 435            RITLREALK 473
nomeodomain-intera protein kinase-lik	Qy 436 HPFFDLLKK 444	

RESULT 2

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A;Molecule type: mRNA
A;Residues: 1-499 <HAN>
A;Residues: 1-499 <HAN>
A;Cross-references: UNIPROT:P49760; GB:L29218; NID:g632967; PIDN:AAA61482.1; PID:g632968
R;Winfield, S.L.; Tayebi, N.; Martin, B.M.; Ginns, E.I.; Sidransky, E.
R;Winfield, S.L.; 12yebi, N.; Martin, B.M.; Ginns, C.I.; Sidransky, E.
A;Title: Identification of three additional genes contiguous to the glucocerebrosidase Ic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      266 FVQSDYTEAYNPKIKRDERTLINPDIKVVDFGSATYDDEHHSTLUSTRHYRAPEVILALG 325
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21-Feb-1992 #sequence_revision 21-Feb-1992 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KRKRNRHCSSHQSRSKSHRRKRSRSIEDDEEGHLICQSGDVLRARYEIVDTLGEGAFGKV
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                    Cjaccesion: A38643 "June 1991 "A R. M. Smith, K.A. Biol. Chem. 266, 3402-3407, 1991 A; Title: Molecular cloning of a novel human cdc2/CDC28-like protein kinase. A; Reference number: A38643; MUID:91139618; PMID:1704889
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                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GDB:126862
A;Map position: 7q31-7q31
(Superfamily: human protein kinase clk1; protein cleared; proposition: protein lockeywords: phosphotransferase
F;129-400/Domain: protein kinase homology «KIN»
                                                                                                                                                                                             A; Accession: A38643
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-454 <JOH>
C; Genetics: CB:M59287
C; Genetics: CB:M59287
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Cipace: OB.Nov-1991 #sequence_revision 08-Nov-1991 #text_change 09-Jul-2004
Cipace: OB.Nov-1991 #sequence_revision 08-Nov-1991 #text_change 09-Jul-2004
Cipace: OB.Nov-1991 #sequence_revision 08-Nov-1991 #text_change 09-Jul-2004
Cipacesion: A39676; S13364
Nol. Cell. Biol. 11, 568-572, 1991
A;Title: STY, a tyrosine-phosphorylating enzyme with sequence homology to serine/threoning A;Reference number: A39676; MUID:91094875; PMID:1986248
A;Accession: A39676
A;Accession: A39676
A;Accession: A39676
A;Accession: A396776
A;Accession: B3364
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A;Accession: A3364

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  284 THTDLKPENILFVKSDYTEAYNPKMKRDERTIVNPDIKVVDFGSATYDDEHHSTLVSTRH 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YRAPEVILALGWSQPCDVWSIGCILIEYYLGFTVFQTHDSKEHLAMMERILGPIPQHMIQ 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KTRKRKYFHHNQLDWDEHSSAGRYVRRRCKPLKEFMLCHDEEHEKLFDLVRRMLEYDPTQ 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: mRNA
A;Residues: 1-378, P', 380-483 <BEN>
A;Residues: experient Fig. 2 is inconsistent with that shown in Fig. 1
A;Note: the sequence from Fig. 2 is inconsistent with that shown in Fig. 1
C;Superfamily: human protein kinase clk1; protein kinase c;Reywords: phosphotransferase; serine/threonine-specific protein kinase
F;158-429/Domain: protein kinase homology <KIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48 HSKTTD---SYYLESRSINEKAYHSRRYVDEYRNDYM-GYEPGHPYGEPGSRYQMHSSKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VQMLEWFDHHGHVCIVFELLGLSTYDFIKENSFLPFQIDHIRQMAYQICQSINFLHHNKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SVRSRRSSPKRK-RNR-HCSSHQSRSKSHRRKRSRSIEDDEEGHLICQSGDVLRARYEIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     127 DTLGEGAFGKVVECIDHGMDGMHVAVKIVKNVGRYREAARSEIQVLEHLNSTDPNSVFRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 HSVEEDTHPSHYLEARSLNERDYRDRRYVDEYRNDYCEGYVPRHYHRDIESGYRIHCSKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
76.2%; Score 1837; DB 2; Length 483;
Best Local Similarity 79.7%; Pred. No. 5.1e-81;
Matches 349; Conservative 32; Mismatches 51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 3
A38643
protein kinase (EC 2.7.1.37) cdc2/cdc28-like - human
C;Species: Homo sapiens (man)
                                                                                                                                                                                                                     protein kinase STY (BC 2.7.1.-) - mou:
N;Alternate names: protein kinase clk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RITLDEALOHPFFDLLKK 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                481
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RITLKEALKHPFFYPLKK
                           |||||||||||||
|HPFFDLLKK 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        307
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Drotein kinase clk3 (EC 2.7.1.-), testis-specific - rat
NyAlternate names: LAWMER kinase
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 21-Apr-1997 #sequence_revision 09-May-1997 #text_change 09-Jul-2004
C;Accession: S70352
B;Becker, W.; Kentrup, H.; Heukelbach, J.; Joost, H.G.
Biochim. Biophys. Acta 1312, 63-67, 1996
A;Title: cDNA cloning and characterization of rat Clk3, a LAWMER kinase predominately expandately expectation: S70352
A;Accession: S70352
A;Molecule type: mRNA
A;Accession: S70352
A;Molecule type: mRNA
A;Accession: S70352
A;Accession: S70352
A;Molecule type: mRNA
A;Accession: S70352
A;Accession: S703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              166 RSEIQVLEHLNSTDPNSVFRCVQMLEWFDHHGHVCIVFELLGLSTYDFIKENSFLPFQID 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             286 VDFGSATYDDEHHSTLVSTRHYRAPEVILALGWSQPCDVWSIGCILIEYYLGFTVFQTHD 345
                                                                                                                                                                                                                                                                                                                                                                                                        91 HRRRSRERGPYRTRKHAHHCHK------RRTRSCSSASSRSQQSSKRSSRED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         319 ADFGSATFDHEHHTTIVATRHYRPPEVILLELGWAQPCDVWSIGCILFEYYRGFTLFQTHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43 PPRRSRSRSHDRLP-----YQRRYRERRDSDTYR---CEERSPSFGEDYYGPSRSR
                                                                                                                                                                                                                                                                                                                                                                  52 HYHRDIESG-YRI-----HCSKSSVRSRRSSPKRKRNRHCSSHQSRSKSHRRKRSRSIED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HIROMAYOI COSINFLHHNKLTHTDLKPENILFVKSDYVVKYNSKMKRDERTLKNTDIKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 346 SKEHLAMMERILGPIPQHMIQKTRKRKYFHHNQLDWDEHSSAGRYVRRCKPLKEFMLCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEEGHLICQSGDVLRARYEIVDTLGEGAFGKVVECIDHGMDGMHVAVKIVKNVGRYREAA
C;Superfamily: human protein kinase clk1; protein kinase homology C;Keywords: alternative splicing; phosphotransferase F;154-433/Domain: protein kinase homology <KIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: clk3
C;Superfamily: human protein kinase clk1; protein kinase homology
C;Keywords: phosphotransferase; protein kinase
F;154-433/Domain: protein kinase homology <KIN>
                                                                                                                       , Score 1321; DB 2; Length 4
, Pred. No. 2e-56;
60; Mismatches 101; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'Match 54.6%; Score 1317; DB 2; Length 4 Local Similarity 55.1%; Pred. No. 3.2e-56; Length 4 tes 250; Conservative 61; Mismatches 101; Indels
                                                                                                                                                                                                                                                 PLEASHSVEEDTHPSHYLEARSLNERDYRDRRYVDEYRNDYCEGYVP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SLEHVQLFDLMRRMLEFDPAQRITLAEALLHPFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        406 DEEHEKLFDLVRRMLEYDPTQRITLDEALQHPFF
                                                                                                                          54.8%;
                                                                                                                                                      Best Local Simitaring ...-
Matches 251; Conservative
                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        226
                                                                                                                 Query Match
Best Local
                                                                                                                       Match
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                                                                                                                                                                                   kina
                                                                                                                                                                                                                                                                                                    A;Description: Phosphorylates Ser, Thr, and Tyr residues on proteins in the spliceosomal (S.Superfamily: human protein kinase old.Kl; protein kinase homology C;Keywords: alternative splicing; phosphotransferase F;161-440/Domain: protein kinase homology <KIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ል
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C;Species: Homo saplens (man)
C;Date: 28-Oct-1996 #sequence_revision 07-Feb-1997 #text_change 09-Jul-2004
C;Accession: S53639; S71040
R;Hanes, J.; von der Kammer, H.; Klaudiny, J.; Scheit, K.H.
A; Mittle: Characterization by cDNA cloning of two new human protein kinases. Evidence ]
                                                                                                                 A;Cross-references: GB:AF023268; NID:g2564910; PIDN:AAC51817.1; PID:g2564911
C;Comment: The short splice form of this protein (see PIR:S53638) lacks the protein
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PEVILALGWSQPCDVWSIGCILIEYYLGFTVPQTHDSKEHLAMMERILGPIPQHMIQKTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KRKY FHHNQLDWDEHSSAGRYVRRCKPLKEFMLCHDEEHEKLFDLVRRMLEYDPTQRIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SRRSSPK--RKRNRHCSSHQSRSKSHRRKRSRSIEDDEEGHLICQSGDVLRARYEIVDTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             130 GEGAFGKVVECIDHGMDGMHVAVKIVKNVGRYREAARSEIQVLEHLNSTDPNSVFRCVQM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LEWFDHHGHVCIVFELLGLSTYDFIKENSFLPFQIDHIRQMAYQICQSINFLHHNKLTHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DIKPENILFVKSDYVVKYNSKMKRDERTLKNTDIKVVDFGSATYDDEHHSTLVSTRHYRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SHYLEARS ----LINERDYRDRRYVDEY-RNDYCEGYVPRHYHRDIESGYRIHCSKSSVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .,
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
A; Reference number: Z16482; MUID: 97474796; PMID: 9331372
                                                                                                                                                                                                                                                                                                                                                                                                                                                          58.8%; Score 1417; DB 2;
59.7%; Pred. No. 5.5e-61;
iive 69; Mismatches 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LDEALQHPFFDLLK 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LGEALOHPFFARLR 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 259; Conservative
                                                                                 A, Molecule type: nucleic acid A, Residues: 1-499 <WIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Accession: S53639
A;Molecule type: mRNA
A;Residues: 1-490 <HAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                  A;Accession: T08825
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                 clk2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                          Function:
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9

Gaps

42;

Length 490;

105

90

43 PPRRSRSRSHDRIP-----YQRRYREHRDSDTYR---CEERSPSFGEDCYGSSRSR

4 PLEASHSVEEDTHPSHYLEARSLNERDYRDRRYVDEYRNDYCEGYVP

ò g ð g

91 HRRKSRERGPÝRTRKHAHHCHK------RRTRSCSSASSRSQGSKRSSRSVED

HYHRDIESG-YRI----HCSKSSVRSRRSSPKRKRNRHCSSHQSRSKSHRRKRSRSIED

25

A;Molecule type: mRNA A;Residues: 1-131,'TG',134-490 <HAW> A;Cross-references: EMBL:L29217; NID:g632971; PIDN:AAA61484.1; PID:g632972

A;Cross-references: UNIPROT:P49761; GB:L29217
KHanes, J.J.; der Kammer, H.; Klaudiny, J.J.; Scheit, K.H.
Submitted to the EMBL Data Library, January 1995
A;Reference number: S71040

A; Accession: S71040

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A;Status: preliminary; translated from GB/EMBL/DDBJ.
A;Modecule type: DNA
A;Residues: 1-903 «ML»
A;Residues: UNIPROT:Q17917; EMBL:Z70205; PIDN:CAA94122.1; GSPDB:GN00028; CESP:E07
A;Cross-references: UNIPROT:Q17917; EMBL:Z70205; PIDN:CAA94122.1; GSPDB:GN00028; CESP:E07
                                   SKSSVRSRRSSPK-----RKRNRHCSSHQSRSKSHRRKRSRSIEDDEEGHLICQSGDVL 119
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345 DSKEHLAMMERILGPIPQHMIQKTRKRKYFHHNQLDWDEHSSAGRYVRRCKPLKEFMLC 404
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A;Accession: T20424
A;Status: preliminary; translated from GB/EWBL/DDBJ
A;Molecule type: DNA
A;Redidues: 1-903 <MIZ.
A;Coss-references: EWBL:568003; PIDN:CAA91979.1; GSPDB:GN00028; CESP:E02H4.3
A;Experimental source: clone E02H4
                                                                                                                                                                                                                                                                             probable protein kinase B02H4.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T19209; T20424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180 PNSVFRCVOMLEWFDHHGHVCIVFELLGLSTYDFIKENSFLPFQIDHIROMAYQICQSIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Map position: X
A;Introns: 512/3; 551/1; 611/2; 641/3; 756/1; 810/2; 839/3; 887/2
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                                                                                                                                     405 HDEEHEKLFDLVRRMLEYDPTQRITLDEALQHPFFDLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Barlow, K. submitted to the EMBL Data Library, November 1995
                                                                                                                                                                                                                                                                                                                                                                                                                submitted to the EMBL Data Library, March 1996 A;Reference number: Z19090 A;Accession: T19209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |:| :: :: ||
SRSGLQASQARPKVPEIVSSQRTQH-
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Best Local Similarity 46.6
Matches 185; Conservative
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Modecule type: mRNA
A,Residues: 1-517 (2111)
A,Cross-references: UNIPROT: P49762; GB:X78715; NID:g472912; PIDN:CAA55367.1; PID:g472913
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein kinase Darkener-of-apricot (EC 2.7.1.-) - fruit fly (Drosophila melanogaster)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RSEIQVLEHLNSTDPNSVFRCVQMLEWFDHHGHVCIVFELLGLSTYDFIKENSFLPFQID 225
                                                                                                                                                              286 VDFGSATYDDEHHSTLVSTRHYRAPEVILALGWSQPCDVWSIGCILIEYYLGFTVFQTHD 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  379 NREHLVYMEKILGPIPSHMIHRTRKQKYFYKGGLVWDENSSDGRYVKENCKPLKSYMLQD 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DDEEGHLICQSGDVLRARYEIVDTLGEGAFGKVVECIDHGMDGMHVAVKIVKNVGRYREA 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    165 ARSEIQVLEHLNSTDPNSVFRCVQMLEWFDHHGHVCIVFELLGLSTYDFIKENSFLPFQI 224
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                                DEEGHLICQSGDVLRARYEIVDTLGEGAFGKVVECIDHGMDGMHVAVKIVKOVGRYREAA 165
                                                                                                                                                                                                                                          226 HIROMAYQICQSINFLHHNKLTHTDLKPENILFVKSDYVVKYNSKMKRDERTLKNTDIKV 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SKEHLLAMMERILGPIPQHMIQKTRKRKYFHHNQLDWDEHSSAGRYVRRRCKPLKEFMLCH 405
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C;Superfamily: human protein kinase clk1; protein kinase homology
C;Keywords: ATP; autophosphorylation; phosphotransferase; protein kinase
F;168-438/Domain: protein kinase homology <KIN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           406 DEEHEKLFDLVRRMLEYDPTQRITLDEALQHPFF 439
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A; Status: preliminar
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OY 224 IDHIROMAYQICOSINFLHHWKITHTDLKPENILFVKSDYVVKY-NSKWKRDERT I	RESULT 11 T04125 protein kinase PK12 (BC 2.7.1), ethylene-induced - common tobacco C;Species: Nicotiana tabacum (common tobacco) C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 16-Aug-2004 C;Accession: T04125 R;Sessa, G.; Raz, V.; Savaldi, S.; Fluhr, R. Plant Cell 8, 2223-223-21 Plant Cell 8, 2223-223-223-21 Plant Cell 8, 2223-223-223-23-23-23-23-23-23-23-23-23-	K.F. Db 1134 Oy 1134 Oy 1134 Oy 1134	Db 165 DYRNHICH/FERIGESLEPFLRKNSYRAPPUDLYREIGROLLECVAFWHDMELIHTDLIND  Qy 254 ENILFYGRADYLKUSKMKRDERTLKNTDIKUVDFGSATYDDEHHSTLUSTR  [
protein kinase STY (EC 2.7.1) [imported] - mouse C.Species: Mus musculus (house mouse) C.Species: Mus musculus (house mouse) C.Date: 02-Jul-1996 #text_change 20-Jun-2000 C.Date: 02-Jul-1996 #text_change 20-Jun-2000 C.Accession: 149068 B. Marius, R.M.; Drmanic, S.; Douville, E.M.; Bell, J.C. J. Biol. Chem. 270, 21524-21531, 1995 A.Title: Alternative splicing of STY, a nuclear dual specificity kinase. A.Accession: 149068; MUID:95394904; PMID:7665564 A.Accession: 149068 MUID:95394904; PMID:9507918 A.Accession: 1396 A.Accession: 1396 A.Accession: 13906 A.Accession: 13907913 A.Accession: 129/3; 160/1; 221/2 C.Keywords: phosphotransferase	Query Match         36.3%; Score 876; DB 2; Length 306;           Best Local Similarity         74.2%; Pred. No. 2.2e-35;           Matches 173; Conservative 21; Mismatches 33; Indels 6; Gaps 4;           Qy         9 HSVEEDTHPSHYLEARSLNERDYRDRRRYDETRNDYCEGYVPRHYHBDIESGYRIHCSKS 68	RESULT 10 T05560 Protein kinase AFC2 (EC 2.7.1) - Arabidopsis thaliana N.Alternate names: protein F22K18.60 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 16-Aug-2004 C;Accssion: T05560 R;Bevan, M.; Wedler, H.; Wedler, E.; Wambutt, R.; Hoheisel, J.; Mewes, H.W.; Mayer, submitted to the Protein Sequence Database, February 1999 A;Reference number: 215419 A;Accession: T05560 A;Molecule type: DNA A;Residues: 1-427 <bev> A;Residues: 1-437 <bev> A;Residues: 34/3; 384/2; 382/3 A;Residues: 34/3; 38/1; 107/1; 158/2; 174/3; 213/1; 243/3; 294/1; 315/3; 348/2; 382/3 A;Retons: 34/3; 98/1; 107/1; 158/2; 174/3; 213/1; 243/3; 294/1; 315/3; 348/2; 382/3</bev></bev></bev></bev></bev></bev></bev></bev></bev></bev></bev></bev></bev></bev></bev></bev>	1 427; 13, Gaps 8; AVKIVKNVGRYRE 163 AVKIVROVKRYRE 137 YDFIKENSFLPFQ 223 YH

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A;Accession: T04460
A;Molecule type: DNA
A;Rosaldues: 1-400 - REDEP>
A;Rosaldues: 1-400 - REDEP>
A;Cross-references: UNITYON Columbia; BAC clone F4D11
C;Genetics:
A;Genetics:
A;Genetics:
A;Gene: ANE3
A;Gene: ANE3
A;Gene: ANE3
A;Gene: ANE3
A;Gene: ANE3
A;Once: F4D11.140
C;Superfamily: protein kinase homology
C;Superfamily: phosphotransferase; protein kinase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TDIKVVDFGSATYDDEHHSTLVSTRHYRAPEVILALGWSQPCDVWSIGCILIEYYLGFTV 340
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32.8%; Score 790; DB 2; Le
Best Local Similarity 41.7%; Pred. No. 3.5e-31;
Matches 169; Conservative 70; Mismatches 134;
A; Reference number: Z15360
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A; Map position: 3
A; Introns: 56/3; 115/1; 124/1; 175/2; 191/3; 230/1; 260/3; 313/1; 334/3; 367/2; 402/3
A; Note: F4P12.70
C; Superfamily: human protein kinase clk1; protein kinase homology
C; Keywords: ATP; phosphotransferase; protein kinase
F; 113-401/Domain: protein kinase homology < KIN>
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N'Alternate names: protein FAD11.140
C'Species: Arabidopsis thaliana (mouse-ear cress)
C'Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 16-Aug-2004
C'Accession: T04460
R'Bevan, M.; Benes, V.; Rechmann, S.; Borkova, D.; Ansorge, W.; Hoheisel, J.; Mewes, submitted to the Protein Sequence Database, April 1998
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A,Residues: 1-467 <KUR>
A,Cross-references: UNIPROT:PS1S66; EMBL:D45354; NID:g642131; PID:g642132
R;Bloecker, H.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Quetier, F.; Salanoubat,
submitted to the Protein Sequence Database, January 2000
A,Reference number: Z23016
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DHIROMAYQICQSINFLHHNKLTHTDLKPENILFVKSDYV----VKYNSKWKRDERTLKN 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----TDIKVVDFGSATYDDEHHSTLVSTRHYRAPEVILALGWSQPCDVWSIGCILIEYYL 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GFTVFQTHDSKEHLAMMERILGPIPQHMIQKT--RKRKYFHHN-QLDWDEHSSAGRYVRR 393
                                                                                                  protein kinase, 54K (EC 2.7.1.-) - Arabidopsis thaliana
N;Alternate names: protein F4Pl2.270
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 19-Mar.1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S71169; T45897
R;Kuromori, T.; Yamanoto, M.
submitted to the EMBL Data Library, January 1995
A;Description: A.thaliana genes encoding protein kinases of a new family.
A;Reference number: S71169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | :|:: |:: |::|::| | ||||||||||| ||:|:
DLVRELGRQLLESVAYMHDLRLIHTDLKPENILLVSSEYIKIPDYKFLSRPTKDGSYFKN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --RCKPLKEFMLCH-DEEHEKLFDLVRRMLEYDPTQRITLDEALQHPFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34.4%; Score 830; DB 2; Length 46 45.8%; Pred. No. 5e-33; tive 71; Mismatches 102; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-467 <BLO>
A;Cross-references: EMBL:AL132966
A;Experimental source: cultivar Columbia; BAC clone F4P12
C;Genetics:
    RFDPSIRMTAHDALRHPFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity *2.0.
Matches 160; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
                                                                                                                                                                                                                                                                                             A; Accession: S71169
                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: T45897
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165

23

105

Length 400;

Indels

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June Kinase homolog protein 1, Lkhl protein - fission yeast (Schizosaccharomyces pombe) C; Species: Schizosaccharomyces pombe C; Species: Schizosaccharomyces pombe C; Species: Schizosaccharomyces pombe C; Species: O2-Apr-2002 #sequence_revision 02-Apr-2002 #text_change 09-Jul-2004 R; Kim, K.H.; Cho, Y.M.; Kang, W.H.; Kim, J.H.; Byun, K.H.; Park, Y.D.; Bae, K.S.; Park, F Biochem. Biophys. Res. Commun. 289, 1237-1242, 2001 A; Title: Negative regulation of filamentous growth and flocculation by Lkhl, a fission yet, A; Accession: JC7794 A; Accession: JC7794 A; Accession: JC7794 A; Accession of filamentous growth and flocculation by Lkhl, a fission yet, A; Accession: JC7794 A; Accession of the dual-specificity protein kinase of the LAWMER if acc. by repressing expression of cell surface proteins for flocculation and morphogenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3;
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396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 31.8%; Score 767; DB 2; Length 57 Local Similarity 41.5%; Pred. No. 6.1e-30; les 141; Conservative 78; Mismatches 115; Indels
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Job time : 44 secs
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Cross-references: EMBL:Z69239; PIDN:CAA93220.1; GSPDB:GN00066; SPDB:SPAC1D4.11c
Experimental source: strain 972h-; cosmid c1D4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       164
                                                             DHIRQMAYQICQSINFLHHNKLTHTDLKPENILFVKSDYVVKYNSKMKRDERTLKNTDIK 284
                                                                                                                                         348 KHIQMLSQQLFKSVAFLHSLGLVHTDLKPENVLLVSNASRTIRLPYRNYSQKVLNSCEIR 407
                                                                                                                                                                                              VVDFGSATYDDEHHSTLVSTRHYRAPEVILALGWSQPCDVWSIGCILIEYYLGFTVFQTH 344
                                                                                                                                                                                                                       345 DSKEHLAMMERILGPIPQHMI---QKTRKRKYFHHNQLDWDEHSSAGRYVR--RRCKPLK 399
                                                                                                                                                                                                                                                                                                  SLIELRVLQTIAHSDPTNENKCIQLRDYFRYHICIVTDLFGWSVPDFLKNNNYIPFFL 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       463 KHIQMLSQQLFKSVAFLHSLGLVHTDLKPENVLLVSNASRTIRLPYRNYSQKVINSCEIR 522
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   345 DSKEHLAMMERILGPIPQHMI----QKTRKRKYFHHNQLDWDEHSSAGRYVR--RRCKPLK 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DDDDGHYKVVPNSKFANRYTVVRLLGHGTFGKVIQCYDQS-TGRHCAIKVTRAIPKYREA 287
                                      165 ARSEIQVLEHLNSTDPNSVFRCVQMLEWFDHHGHVCIVFELLGLSTYDFIKENSFLPFQI 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ARSEIQVLEHLNSTDPNSVFRCVQMLEWFDHHGHVCIVFELLGLSTYDFIKENSFLPFQI 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DHIRQMAYQICQSINFLHHNKLTHTDLKPENILFVKSDYVVKYNSKWKRDERTLKNTDIK 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Species: Schizosaccharomyces pombe bate: 03-Dec-1999 #text_change 18-Aug-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DDEEGHLICOSGDVLRARYEIVDTLGEGAFGKVVECIDHGMDGMHVAVKIVKNVGRYREA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gane: SPDB:SPAC1D4.11c
A;Map position: 1
C;Superfamily: yeast probable protein kinase KNS1; protein kinase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Juye, G.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V. ubmitted to the EMBL Data Library, February 1995.
;Reference number: Z21765
;Accession: T38052
;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78; Mismatches 115; Indels
                                                                                                                                                                                                                                                                                                                                                                              528 QIFAVSSPEVALLLDLLKKVFVYDPKRRITAKEALWHPFF 567
                                                                                                                                                                                                                                                                                                                                                        EFMLCHDEEHEKLFDLVRRMLEYDPTQRITLDEALQHPFF 439
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Pred. No. 7.1e-30;
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31.8%;
Best Local Similarity 41.5%;
Matches 141; Conservative 71
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14615, A 1763, Ap 2391, Ap

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16, Appl 47, Appl 418, Appl 112, Appl 343, App 352, App 118, App 111, Appl 27, Appl 27, Appl

Sequence Seq

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Run on:

Sequence:

Searched:

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AFGKVVECIDHGMDGMHVAVKIVKNVGRYREAARSEIQVLEHLNSTDPNSVFRCVQMLEW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FDHHGHVCIVFELLGLSTYDFIKENSFLPFQIDHIRQMAYQICQSINFLHHNKLTHTDLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ILALGWSQPCDVWSIGCILIEYYLGFTVFQTHDSKEHLAMMERILGPIPQHMIQKTRKRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEPLICANT: PLEXXIVON, INC.

TITLE OF INVENTION: MOLECULAR SCAFFOLDS FOR KINASE LIGAND DEVELOPMENT
FILE REFERENCE: 039363-1703

CURRENT APPLICATION NUMBER: PCT/US04/30360

CURRENT FILING DATE: 2004-09-15

PRIOR FILING DATE: 2003-09-15

NUMBER OF SEQ ID NOS: 167

SOFTWARE: PATCHLING DATE: 2003-09-15

LENUMBER: SECOLUL OF SEQ ID NOS: 167

LENUMBER: SECOLUL OF 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 374;
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PCT-USO4-42360-345
PCT USO4-42360-354
PCT USO4-30360-16
PCT-USO4-30360-18
US-10-450-763-41854
PCT-USO4-30360-118
PCT-USO4-42360-343
PCT-USO4-42360-352
WS-11-021-951-188
PCT-USO4-30360-111
PCT-USO4-30360-111
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PCT-USO4-30360-111
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Best Local Similarity 84.7%; Pred. No. 1.4e-101;
Matches 315; Conservative 24; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                     PCT-US04-42360-1763
FCT-US04-42360-2391
US-60-643-717-10080
PCT-US04-30360-98
US-11-033-515-12
US-11-033-515-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALIGNMENTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Unknown Organism
     PCT-US04-30360-133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 1
PCT-US04-30360-133
                                                       313
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Sequence 134, App
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Sequence 135, App
Sequence 136, App
Sequence 35, Appl
Sequence 46352, A
Sequence 60, Appl
Sequence 187, Appl
Sequence 187, Appl
Sequence 171, Appl
Sequence 171, Appl
Sequence 1761, Appl
Sequence 2389, Appl
Sequence 2389, Appl
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3: /cgn2 - /cptodata/1/paa/USO7 NEW COMB.pep:*

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Sequence 2, Application US/10878630A
GENERAL INFORMATION:
APPLICANT: Wisotzkey, Robert G.
TITLE OF INVENTION: CDC29-Like protein kinase CLK3 disruptions, compositions and TITLE OF INVENTION: CDC29-Like protein kinase CLK3 disruptions, compositions and TITLE OF INVENTION: CDC39-Like protein thereto
TITLE OF INVENTION: MADRER: US/10/878,630A
CURRENT FILING DATE: 2004-66-28
PRIOR FILING DATE: 2003-66-26
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin version 3.3
SEQ ID NO 2.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              174 HLNSTDPNSVFRCVQMLEWFDHHGHVCIVFELLGLSTYDFIKENSFLPFQIDHIRQMAYQ
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CURRENT APPLICATION WAMBER: PCT/USO4/30360
CURRENT FILING DATE: 2004-09-15
PRIOR APPLICATION NUMBER: 60/503,277
WUMBER OF SEQ ID NOS: 167
SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 490;
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55.6%; Pred. No. 5.4e-77;
ive 62; Mismatches 110;
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DLMRRMLEFDPAQRITLAEALLHPFF 472
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; Sequence 134, Application PC/TUS0430360
; Septembl. INFORMATION:
; APPLICANT: PLEXXIKON, INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 55.6
Matches 248; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Mus musculus
                                                 US-10-878-630A-2
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                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 490
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LOCATION: (271).. (290)
OTHER INFORMATION: TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE domain identified
OTHER INFORMATION: by eMATRIX, accession number PR00109B, p-value=7.559e-10, raw scc
OTHER INFORMATION: of 12.27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (155)..(470)
OTHER INFORMATION: Bukaryotic protein kinase domain identified by PFam,
OTHER INFORMATION: accession name pkinase, E-value=4.8e-69, PFam score of 242.8
301 YFHHDRLDWDEHSSAGRYVSRACKPLKEFMLSQDVEHERLFDLIQKMLEYDPAKRITLRE 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84 HCSSHQSRSKS-HRRKRSRSIEDDEEGHLICQSGDVLRARYEIVDTLGEGAFGKVVECID 142
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59.8%; Pred. No. 2.8e-77;
ive 59; Mismatches 89; Indels 21;
                                                                                                                                                                                                                                                                 APPLICATION TOWNER TOWNER TOWNER AND POLYPEPTIDES TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES FILE OF INVENTION NUMBER: US/10/450,763
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR FILING DATE: 2001-03-30
PRIOR PILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: CUSTOM
SEQ ID NO 53713
LENGTH: 490
                                                                                                                                                                                                                          Sequence 53713, Application US/10450763 GENERAL INFORMATION:
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361 ALKHPFFDLLKK 372
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Matches 251; Conservative
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ORGANISM: Homo sapiens
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     427
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                                                                                                                                                                                                                                          315 ALGWSOPCDVWSIGCILIEYYLGFTVFOTHDSKEHLAMMERILGPIPOHMI-OKTRKRKY 373
                                                                                                                                                                                                                                                                                                                                                                            ----HNQLDWDEHSSAGRYVRRRCKPLKEFMLCHD 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    395 FEKLPDGTWSLKKTKDGKREYKPPGTRKLHNILGVETGGPGGRRAGESGHTVADYL---- 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LGWPLYPGASEYDQIRYISQTQGLPAEYLLSAGTKTTRFFNRDTDSPYPLWRLKTPDDHE 307
                                                                                                  NILFVKSDYVVKYNSKMKRDERTLKNTDIKVVDFGSATYDDEHHSTLVSTRHYRAPEVIL 314
173 VVKAYDR-VEQEWVAIKIIKNKKAFLNQAQIEVRLLELMNKHDTEMKYYIVHLKRHFMFR 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100 SRSIEDDEEGHLICQSGDVLRA---RYEIVDTLGEGAFGKVVECIDHGMDGMHVAVKIVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         157 NVGRYREAARSEIQVLEHINSTDPNSVPRCVOMLEWFDHHGHVCIVFELLGLSTYDFIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         217 NSFLPFQIDHIRQMAYQICQSINFLHHNKLTHTDLKPENILFVKSDYVVKYNSKMKRDER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        386 S-----AGRYVRRRCKPLKEF------MLCHDEEHEKLFDLVRRMLEYDFTQR
                                                                  197 GHVCIVFELLGLSTYDFIKENSFLPFQIDHIRQMAYQICQSINFLHHNKLT--HTDLKPE
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TITLE OF INVENTION: MOLECULAR SCAFFOLDS FOR KINASE LIGAND DEVELOPMENT
FILE OF INVENTION: MOLECULAR SCAFFOLDS FOR KINASE LIGAND DEVELOPMENT
FILE REFERENCE: 039563-1703
CURRENT APPLICATION WINBER: PCT/US04/30360
CURRENT FILING DATE: 2004-09-15
PRIOR APPLICATION NUMBER: 60/503,277
NUMBER OF SEQ ID NOS: 167
SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----KFKDLILRMLDYDPKTRIQPYYALQHSFF 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               407 EEHEKLFDLVRRMLEYDPTQRITLDEALQHPFF
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Best Local Similarity 29.4%;
Matches 109; Conservative 79
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ORGANISM: Unknown Organism
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CURRENT APPLICATION NUMBER: PCT/USO4/42360
CURRENT APPLICATION NUMBER: 60/531,341
PRIOR PILING DATE: 19-Dec-2003
NUMBER OF SEQ ID NOS: 2587
SOFTWARE: Perl script
SEQ ID NO 2024
LENGTH: 763
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GKVVECIDHGMDGMHVAVKIVKNVGRYREAARSEIQVLEHLNSTDPNSVFRCVQMLEWFD 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |:||:||: | :: ||:||:||:||:|| GQVVKAYDR-VEQEWAIKIIKNKKAFLNQAQIEVRLIELBLANKHDTEMKYYIVHIKRHFM 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PENILFVKSDYVVKYNSKMKRDERTLKNTDIKVVDFGSATYDDEHHSTLVSTRHYRAPEV 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PENILLCNP------KRSAIKIVDFGSSCQLGQRIYQYIQSRFYRSPEV 224
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                                                                                                                                                                                                                                                                                                                                                                                                               79 RKRNRHCSSHQSRSKSHRRKRSRSI----EDDEEGHLICQSGDVLRARYEIVDTLGEGAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HHGHVCIVFELLGLSTYDFIXENSFLPFQIDHIRQMAYQICQSINFLHHNKLT--HTDLK
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                                                                                                                                                                                                                                   19.6%; Score 473.5; DB 1; Length 421; 29.4%; Pred. No. 1.8e-23; Live 71; Mismatches 145; Indels 63
                                                                                                  ) OTHER INFORMATION: Description of Unknown Organism: Mammalian; OTHER INFORMATION: protein sequence
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Best Local Similarity 29.5%; Pred. No. 3.8e-23;
Matches 116; Conservative 72; Mismatches 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   405 HDEEHEKLFDLVRRMLEYDPTQRITLDEALQHPFF 439
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DATABASE ACCESSION NUMBER: Refseq / NP_036923
DATABASE ENTRY DATE: 2003-10-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2024, Application PC/TUS0442360 GENERAL INFORMATION:
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       TYPE: PRT
ORGANISM: Unknown Organism
FEATURE:
                                                                                                                                                                                                                                                                                                             Conservative
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hes 116; Conserv
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979 VIVMSTINPIKDLIADLIGCORLPEDORKKVHOLKDLIDQILMLDPAKRISINQALQHAF 1038
                                                                                                                                                                          217 NSFLPFQIDHIRQMAYQICQSINFLHHNKLTHTDLKPENILFVKSDYVVKYNSKMKRDER 276
                                                                                                                                                                                                                                                      335 YLGFTVFQTHDSKEHLAMMERILGPIPQHMIQK-TRKRKYFHHN----QLDWDEHSSAGR 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83 IRNNELMOKTGLKELEFLKKLNDADPDDKFHCLRLFRHFYHKQHLCLVFEPLSMNLREVI 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         143 KKYGKDVGLHİKAVRSYSQÖLFLALKLİKRCNILHADİKPDNİLVNES------ 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 332 IEYYLGFTVFQTHDSKEHLAMMERILGPIPQHMIQK-TRKRKYFHHN----QLDWDEHSS 386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               274 DERTLKNTDIKVVDFGSATY--DDEHHSTLVSTRHYRAPEVILALGWSQPCDVWSIGCIL 331
                                                                                                                                        277 TLKNTDIKVVDFGSATY--DDEHHSTLVSTRHYRAPEVILALGWSQPCDVWSIGCILIEY
                                                                                                                                                                                                                                                                                                                                                              390 Y-VRRRCKPLKEFM-----LCHDEEHE--KLFDLVRRMLEYDPTQRITLDEALQHPF
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Sequence 136, Application PC/TUS0430360
GENERAL INFORMATION:
APPLICANT: PLEXXIXON, INC.
TITLE OF INVENTION: MOLECULAR SCAFFOLDS FOR KINASE LIGAND DEVELOPMENT
FILE REFERENCE: 039363-1703
CURRENT APPLICATION NUMBER: PCT/US04/30360
CURRENT PILING DATE: 2004-09-15
PRIOR APPLICATION NUMBER: 60/503,277
PRIOR APPLICATION NUMBER: 60/503,277
NUMBER OF SEQ ID NOS: 167
SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Description of Unknown Organism: Mammalian ; OTHER INFORMATION: protein sequence PCT-US04-30360-136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 371;
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17.4%; Score 419.5; DB 1; Length 3
Best Local Similarity 29.5%; Pred. No. 4.6e-20;
Matches 107; Conservative 73; Mismatches 142; Indels
                                                            818 GKDVGLHIKAVRSYSQQLFLALKLLKRCNILHADIKPDNILVNES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Unknown Organism
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      101 RSIED---DEEGHLICQSGDVLRARYEIVDTLGEGAFGKVVECIDHGMDGMHVAVKIVKN 157
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CURRENT PILING DATE: 2005-02-04
PRIOR PILING DATE: 2005-02-04
PRIOR FILING DATE: 2002-03-14
PRIOR FILING DATE: 2001-03-14
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/276,025
PRIOR PILING DATE: 2001-09-26
PRIOR PILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/314,967
PRIOR FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/314,967
PRIOR FILING DATE: 2001-09-10
PRIOR FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/315,102
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/315,102
PRIOR APPLICATION NUMBER: 60/315,102
PRIOR APPLICATION NUMBER: 60/313,580
PRIOR APPLICATION NUMBER: 60/313,580
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SOCTWARR: FastSEQ for Windows Version 4.0
SEQ ID NO 258
LENGTH: 1043
                                                                                                                                                                                            Sequence 258, Application US/11050926
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Karen LU
Rosemarie SCHMANDT
Xumei ZHAO
Karen GLATT
                                                                                                                                                                                                                                                APPLICANT: JOHN MONAHAN
APPLICANT: Manjula GANNAVARAPU
APPLICANT: Sebaetian HOERSCH
APPLICANT: Shubhangi KAMATKAR
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Robert C. BAST, Jr.
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Rachel E. MEYERS
Michael MORRISEY
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Best Local Similarity 26.2*
Matches 126; Conservative
428 ITLDEALQHPF 438
                                                      ITPIETLNHPF 378
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; ORGANISM: Homo sapiens
US-11-050-926-258
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350 LAMMERILGPIPQHMIQKTRKRKYFHHNQLDWDEHSSAGRYVRRRCKPLKEFMLCHDEEH 409
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                                                                                                             US-10-450-763-46352
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                                                                                                                                       Query Match
Best Local'S
Matches 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               346 -SKEHLAMMERILGPIPQHMIQKTRKRKYFHHNQLDWDEHSSAGRYVRRCKPLK---- 399
                                                                                                                                                                                                                                                                                                                                  121 ARYEIVDTLGEGAFGKVVECIDHGMDGMHVAVKIVKNVGRYREAARSEIQVLEHLNSTDP 180
                                                                                                                                                                                                                                                                                                                                                                                        N----SVFRCVQMLEWFDHHG----HVCIVFELLGLSTYDFIXENSFLPFQIDHIRQMA 231
                                                                                                                                                                                                                                                                                                                                                                                                                                             232 YQICQSINFLHHN-KLTHTDLKPENILFVKSDYVVKYNSKMKRDERTLKNTDIKVVDFGS 290
                                                                                                                                                                                                                                                                                                                                                   19 ARYILVRKIGMGHFSTVWLAKDM-VNNTHVAMKIVRGDKVYTEAAEDEIKLLQRVNDADN 77
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                                                                                                                                                                                                                                                                                                        52; Gaps
                           APPLICANT: PLEXXIKON, INC.

TITLE OF INVENTION: MOLECULAR SCAFFOLDS FOR KINASE LIGAND DEVELOPMENT FILE REFERENCE: 039393-1703
CURRENT APPLICATION NUMBER: PCT/US04/30360
CURRENT FILING DATE: 2004-09-15
PRIOR PPLICATION NUMBER: 60/503,277
PRIOR PILING DATE: 2003-09-15
NUMBER OF SEQ ID NOS: 167
SOFTWARE: PATENTIN Ver. 3.2
                                                                                                                                                                                                          FRATURE:

OTHER INFORMATION: Description of Unknown Organism: Mammalian

OTHER INFORMATION: protein sequence

PCT-USO4-30360-35
                                                                                                                                                                                                                                                                              Length 373;
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                                                                                                                                                                                                                                                                            15.8%; Score 380; DB 1; Length 37 Similarity 27.9%; Pred. No. 1.6e-17; 96; Conservative 70; Mismatches 126; Indels
Sequence 35, Application PC/TUS0430360 GENERAL INFORMATION:
                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Unknown Organism
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ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                     SEQ ID NO 35
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Sequence 8, Application PC/TUSO503526
Sequence 8 Application PC/TUSO503526
GENERAL INFORMATION:
APPLICANT: EXELIXIS. INC.
TITLE OF INVENTION: MBMS AS MODIFIERS OF BRANCHING MORPHOGENESIS AND METHODS OF USE
FILE REFERENCE: EXO5-003C-PC
CURRENT APPLICATION NUMBER: PCT/USO5/03526
CURRENT FILING DATE: 2005-01-27
PRIOR FILING DATE: 2004-01-28
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PATENTIN VETSION 3.2
SEQ ID NO 8
LOCATION: (622)..(653)

OTHER INFORMATION: Protein kinases ATP-binding region proteins domain identified OTHER INFORMATION: Protein kinases ATP-binding region proteins domain identified OTHER INFORMATION: Score of 18.39

FEATURE:
NAME/KEY: DOMAIN
LOCATION: (507)..(674)

OTHER INFORMATION: Extravotic protein kinase domain identified by FFam,
OTHER INFORMATION: accession name pkinase, B-value=3.5e-27, PFam score of 101.9
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                                                                                                                                                                                                                                                                                                                                                                                                                                      176 NSTDPNSVFRCVQMLEWPDHHGHVCIVFELLGLSTYDFIKE--NSFLPFQIDHIRQMAYQ
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                                                                                                                                                                                                                                                                                               th 14.0%; Score 337; DB 6; Length 703; Similarity 32.7%; Pred. No. 1.7e-14; 65; Conservative 47; Mismatches 69; Indels
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--QASVKVIDFGSSCYEHQ 661
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ORGANISM: Homo sapiens
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377 NQLDWDEHSSAGRYVRRCK-PLKEFMLCHDEEHEKLFDLVRRMLEYDPTQRITLDEALQ 435
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     INVENTION: New Biological Entities And The Pharmaceutical INVENTION: And Diagnostic Use Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 359;
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TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: '90CIP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30
PRIOR FILING DATE: 2000-03-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 13.5%; Score 326.5; DB 7; Best Local Similarity 26.9%; Pred. No. 4.1e-14; Matches 98; Conservative 66; Mismatches 129;
                                                   FILE REFERENCE: 04156.0002U5
CURRENT APPLICATION NUMBER: US/11/021,951
CURRENT FILING DATE: 2004-12-22
                                                                                                    CURRENT FILING DATE: 2004-12-22
PRIOR APPLICATION NUMBER: 10/872,198
PRIOR FILING DATE: 2004-06-18
PRIOR FILING DATE: 2004-06-18
PRIOR FILING DATE: 2004-02-11
PRIOR FILING DATE: 2004-02-11
PRIOR PLICATION NUMBER: 60/524,960
PRIOR PELING DATE: 2003-11-25
PRIOR APPLICATION NUMBER: EP 04003058
PRIOR FILING DATE: 2003-11-11
PRIOR FILING DATE: 2003-11-11
PRIOR PILING DATE: 2003-11-11
PRIOR PILING DATE: 2003-11-10
PRIOR PILING DATE: 2003-11-10
PRIOR PILING DATE: 2003-11-10
PRIOR PILING DATE: 2003-11-10
PRIOR PILING DATE: 2003-11-10
PRIOR PILING DATE: 2003-06-18
NUMBER OF SEQ ID NOS: 191
SEQ ID NO 187
LENGTH: 359
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US-11-021-951-187
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TITLE OF INVENTION: MOLECULAR SCAFFOLDS FOR KINASE LIGAND DEVELOPMENT
FILE REFERENCE: 039363-1703
CURRENT APPLICATION NUMBER: PCT/US04/30360
CURRENT FILING DATE: 2004-09-15
PRIOR APPLICATION NUMBER: 60,563,277
PRIOR FILING DATE: 2003-09-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13.5%; Score 326.5; DB 1; Length 358; larity 26.9%; Pred. No. 4.1e-14; Conservative 64; Mismatches 131; Indels 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Description of Unknown Organism: Mammalian; OTHER INFORMATION: protein sequence
220 LFTIQKVLGPLPSEQMKLFYSNPRFHGLRFPAVNHPQS---LERRYLGIL-
                                                                                                               268 SVLLDLMKNLLKIDPADRYLTEQCLNHPTF 297
                                                                                 410 EKLFDLVRRMLEYDPTQRITLDEALQHPFF 439
                                                                                                                                                                                                                                                                   Sequence 60, Application PC/TUS0430360 GENERAL INFORMATION:
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US-11-021-951-187
Sequence 187, Application US/11021951
GENERAL INFORMATION:
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APPLICANT: KOLTERMANN, Andre
APPLICANT: SCHEIDIG, Andreas
APPLICANT: VOTSMEIER, Christian
APPLICANT: Kettling, Ulrich
APPLICANT: COCO, Wayne Michael
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ORGANISM: Unknown Organism
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SOFTWARE: PatentIn Ver. 3.2
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Best Local Similarity
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HAYF 308
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LOCATION: (260)...(291)

OTHER INFORMATION: Protein kinases ATP-binding region proteins domain identified
OTHER INFORMATION: by eMATRIX, accession number BL00107A, p-value=4.375e-21, raw
US-10-450-763-44291
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TITLE REPERENCE: 033963-1703
FILE REFERENCE: 033963-1703
CURRENT APPLICATION NUMBER: PCT/US04/30360
CURRENT FILING DATE: 2004-09-15
PRIOR APPLICATION NUMBER: 60/503,277
PRIOR PILING DATE: 2003-09-15
NUMBER OF SEQ ID NOS: 167
SOFTWARE: PATENTIN VET. 3.2
SEQ ID NO 17
LENGTH: 359
                                                                                                                                                                                                                                                                                                                                            71;
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                                                                                                                                                                                                                                                                                                     Query Match 13.5%; Score 326.5; DB 6; Length Best Local Similarity 26.9%; Pred. No. 5.5e-14; Matches 98; Conservative 64; Mismatches 131; Indels
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PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: CUSTOM
SEQ ID NO 44291
LENGTH: 480
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HAYF 428
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Score 323.5; DB 1; Length 359; Pred. No. 6.4e-14;

13.4%;

Query Match Best Local Similarity

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149 HVAVK-----IVKNVGRYREAARSEIQVLEHL---NSTDPNSVFRCVQMLEWFDHHG 197
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89 OSRSKSHRRKRSRSIEDDEEGHLICQSGDVLRARYEIVDTLGEGAFGKVVECIDHGMDGM 148
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Job time : 30 secs
                             156 AVNED-----
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